

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 14:19:51 ; Search time 18.65 Seconds
(without alignments)
1621.345 Million cell updates/sec

Title: US-08-883-036a-2

Perfect score: 440
Sequence: 1 MEORGONAPASGARKRHGP.....HLSSGKFMYLEGNADMSMS 440

Scoring table: OLIGO
Gapop 60.0 , Gapept 60.0

Searched: 198801 seqs, 68722935 residues

Word size : 6

Total number of hits satisfying chosen parameters: 1674

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	1.8	29	2	T03653 phospholipid trans
2	8	1.8	121	2	T04093 choline dehydrat
3	8	1.8	592	2	T51712 NADH dehydrogenase
4	8	1.8	598	2	D71391 BOLFI protein - hu
5	8	1.8	1239	1	Q08E10 rex protein - siml
6	7	1.6	39	2	S44288 adipoiketic hormo
7	7	1.6	61	1	AKI012 hypothetical prote
8	7	1.6	73	2	S04874 30s ribosomal prot
9	7	1.6	89	2	B81179 hypothetical prote
10	7	1.6	103	2	C69000 13K sin operon hyp
11	7	1.6	111	2	B25159 Ig heavy chain V r
12	7	1.6	115	2	S36284 hypothetical prote
13	7	1.6	123	2	F83716 probable lpgs prot
14	7	1.6	130	2	A27632 conserved hypothet
15	7	1.6	132	2	C72200 cytochrome oxidase
16	7	1.6	146	2	S56158 probable integral
17	7	1.6	152	2	T36081 hypothetical prote
18	7	1.6	151	2	T03898 micrococcal nuclea
19	7	1.6	165	2	T03898 probable blrb prot
20	7	1.6	174	1	NCB8PX lipid-transfer-lik
21	7	1.6	181	2	T47408 NAD(P)H oxidoreduc
22	7	1.6	193	2	C69779 peptidylprolyl iso
23	7	1.6	197	2	C69779 hypothetical prote
24	7	1.6	204	2	T21587 pilo protein - Nel
25	7	1.6	213	2	S27736 ribonuclease (EC 3
26	7	1.6	213	2	S70837 hypothetical prote
27	7	1.6	233	2	S71464 N-(5'-phospho-D-ri
28	7	1.6	238	2	H75392
29	7	1.6	243	2	G81255

30	7	1.6	243	2	S44914
31	7	1.6	246	2	A69013
32	7	1.6	249	2	D69065
33	7	1.6	251	2	C72572
34	7	1.6	261	2	F83833
35	7	1.6	275	2	A82578
36	7	1.6	293	2	A49539
37	7	1.6	297	1	H64783
38	7	1.6	308	2	F69203
39	7	1.6	310	1	G70330
40	7	1.6	319	2	S30173
41	7	1.6	326	2	H83746
42	7	1.6	326	2	A59241
43	7	1.6	328	2	D83275
44	7	1.6	329	2	D71887
45	7	1.6	330	2	C64627
46	7	1.6	333	2	JC2329
47	7	1.6	337	2	C81801
48	7	1.6	337	2	F81066
49	7	1.6	346	2	A82502
50	7	1.6	348	2	T50107
51	7	1.6	362	2	T45898
52	7	1.6	371	2	B39625
53	7	1.6	379	2	S49614
54	7	1.6	393	2	T36842
55	7	1.6	397	2	D75387
56	7	1.6	397	2	A39565
57	7	1.6	399	2	A39625
58	7	1.6	413	2	T05228
59	7	1.6	415	2	T36906
60	7	1.6	420	2	T47868
61	7	1.6	428	2	T44596
62	7	1.6	431	2	H70555
63	7	1.6	435	2	T01805
64	7	1.6	436	1	S49458
65	7	1.6	437	2	A69128
66	7	1.6	451	2	H75627
67	7	1.6	459	2	T17141
68	7	1.6	463	2	H72771
69	7	1.6	463	2	T48116
70	7	1.6	476	2	T27051
71	7	1.6	478	2	T08395
72	7	1.6	482	2	T08256
73	7	1.6	485	2	A71266
74	7	1.6	488	2	S71029
75	7	1.6	507	2	T19136
76	7	1.6	520	2	F69470
77	7	1.6	521	2	B82127
78	7	1.6	522	2	B71807
79	7	1.6	523	2	S55677
80	7	1.6	524	2	A54856
81	7	1.6	524	2	T38560
82	7	1.6	535	2	T38433
83	7	1.6	539	2	F70737
84	7	1.6	557	2	S38908
85	7	1.6	558	2	A33616
86	7	1.6	575	2	G75282
87	7	1.6	588	2	D72062
88	7	1.6	593	2	T30658
89	7	1.6	624	2	T00044
90	7	1.6	628	2	T19316
91	7	1.6	647	2	G71490
92	7	1.6	649	2	T18063
93	7	1.6	657	2	A83460
94	7	1.6	669	2	T14725
95	7	1.6	670	2	A75542
96	7	1.6	674	2	G70875
97	7	1.6	709	2	F75584
98	7	1.6	725	2	B82425
99	7	1.6	725	2	T04792
100	7	1.6	774	1	S37606
101	7	1.6	798	2	T00131
102	7	1.6	801	2	T29018

ZK688.7 protein - conserved hypothet
conserved hypothet
hypothetical prote
ABC transporter (A
glycerol uptake fa
xyloglucan endo-1,
carbamate kinase (
5-methyltetrahydro
ADPglyceromanno-he
probable mercuic
acetoin dehydrogen
DNA-directed DNA p
DNA polymerase III
ADPglyceromanno-he
ADPglyceromanno-he
translation Initia
ketol-acid reducto
ketol-acid reducto
oxloreductase, Gf
MHC class I histoc
diaminopimelate ep
T-cell receptor al
cych protein - Rhl
probable secreted
NADH dehydrogenase
lymphoid enhancer-
T-cell receptor al
hypothetical prote
probable Integral
hypothetical prote
26S proteasome reg
probable transmem
hypothetical prote
pyrophosphate--fru
aspartate--tRNA II
probable sensor hI
NADH dehydrogenase
hypothetical prote
hypothetical prote
UTP-glucose glucos
cytochrome d ubiq
probable transcrip
flak protein - Vib
hypothetical prote
dipeptide ABC tran
sulfate permease f
DNA repair protein
glutamate transport
high affinity glut
glutamate transport
excitatory amino a
chaperonin groEL1
glutathione reduct
heterogeneous ribo
probable glutathio
single-stranded-DN
hypothetical prote
vacuolar sorting r
hypothetical prote
hypothetical prote
DNA binding protei
cytochrome C-type
hypothetical prote
conserved hypothet
probable oxidoreduc
hypothetical prote
conserved hypothet
hypothetical prote
SEC18 protein - ye
xylan 1,4-beta-xy1
hypothetical prote

103	7	1.6	838	2	T13102	probable minor tail
104	7	1.6	875	2	C81209	tsPA protein NMB03
105	7	1.6	880	2	G81786	Neisseria-specific
106	7	1.6	956	1	R8HMSC	probable RNA-direct
107	7	1.6	1108	2	E71104	probable cell divi
108	7	1.6	1110	2	T33877	hypothetical prote
109	7	1.6	1116	2	A27826	DNA-directed RNA p
110	7	1.6	1245	1	VHMW82	structural polypor
111	7	1.6	1346	2	T17412	polyketide synthas
112	7	1.6	1525	1	A56699	guanylate cyclase
113	7	1.6	1539	2	T48059	ABC transporter-1i
114	7	1.6	2067	2	A42854	probable spindle p
115	7	1.6	2204	1	R8NZNV	genome polyprotein
116	7	1.6	2325	1	A61208	chondroitin sulfat
117	7	1.6	3054	1	GNEVEV	genome polyprotein
118	7	1.6	3390	1	GNMVD3	genome polyprotein
119	6	1.4	15	2	S59492	formate dehydrogen
120	6	1.4	43	2	A81532	hypothetical prote
121	6	1.4	46	2	A60495	T-cell receptor be
122	6	1.4	50	2	D72804	cathepsin E (EC 3.
123	6	1.4	50	2	C34643	phosphoenolpyruvat
124	6	1.4	56	2	JM0072	myosin alkali ligh
125	6	1.4	59	2	S25629	hypothetical prote
126	6	1.4	62	2	E84008	hypothetical 7.5k
127	6	1.4	63	2	JN0733	hypothetical 7.5k
128	6	1.4	63	2	A58511	bruoconitryphan pr
129	6	1.4	65	2	S14712	hypothetical prote
130	6	1.4	71	2	B64479	hypothetical prote
131	6	1.4	72	2	A75099	hypothetical prote
132	6	1.4	73	2	J50514	hypothetical 7.5k
133	6	1.4	74	1	HHSY34	heat shock protein
134	6	1.4	74	2	B40513	hypothetical prote
135	6	1.4	78	2	D82110	conserved hypotet
136	6	1.4	79	2	T22435	hypothetical prote
137	6	1.4	79	2	T36418	hypothetical prote
138	6	1.4	81	2	JN0058	hypothetical 8.9k
139	6	1.4	82	2	T06236	probable 3,4-dihyd
140	6	1.4	82	2	T30649	hypothetical prote
141	6	1.4	84	2	D70672	hypothetical prote
142	6	1.4	85	1	IMECP3	immunity protein -
143	6	1.4	87	2	B82678	hypothetical prote
144	6	1.4	89	2	T52484	ribosomal protein
145	6	1.4	90	2	T31980	hypothetical prote
146	6	1.4	91	2	E75531	ribosomal protein
147	6	1.4	92	2	A40533	CAMP-dependent pro
148	6	1.4	95	2	T10931	ribosomal protein
149	6	1.4	96	2	G83084	Glu-tRNA(Gln) amid
150	6	1.4	99	2	T21919	hypothetical prote
151	6	1.4	100	2	S76444	transposase slr016
152	6	1.4	100	2	S76090	transposase slr1016
153	6	1.4	102	2	S69877	hypothetical prote
154	6	1.4	102	2	F75077	hypothetical prote
155	6	1.4	102	2	T10878	y4lb protein - Rhi
156	6	1.4	102	2	C75520	hypothetical prote
157	6	1.4	102	2	B72652	hypothetical prote
158	6	1.4	103	2	A26736	transformation-ind
159	6	1.4	103	2	I50417	RSV-induced protei
160	6	1.4	103	2	A72772	hypothetical prote
161	6	1.4	105	2	C64571	hypothetical prote
162	6	1.4	105	2	T37176	hypothetical prote
163	6	1.4	106	2	F69055	conserved hypotet
164	6	1.4	107	2	PL0270	ig kappa chain V r
165	6	1.4	107	2	PL0271	ig kappa chain V r
166	6	1.4	107	2	PL0272	ig kappa chain V r
167	6	1.4	107	2	T35523	probable small sec
168	6	1.4	107	2	H82558	hypothetical prote
169	6	1.4	108	2	J01428	hypothetical 11.6k
170	6	1.4	109	2	T02716	acidic ribosomal p
171	6	1.4	110	2	T02039	acidic ribosomal p
172	6	1.4	110	2	T02039	hypothetical prote
173	6	1.4	111	2	B45824	fla1 protein - Bac
174	6	1.4	113	2	T30436	hypothetical prote
175	6	1.4	114	1	R3HS2H	ribosomal protein
176	6	1.4	114	2	E48364	hypothetical prote
177	6	1.4	115	1	MMRCP3	12K protein - pota
178	6	1.4	115	2	J02236	hypothetical 12.4k
179	6	1.4	115	2	T35387	hypothetical prote
180	6	1.4	116	1	R5HSH9	ribosomal protein
181	6	1.4	116	1	A83504	hypothetical prote
182	6	1.4	117	2	T43941	ribosomal protein
183	6	1.4	117	2	A37165	sporulation locus
184	6	1.4	117	2	A71063	hypothetical prote
185	6	1.4	119	2	T17003	dormancy-associate
186	6	1.4	119	2	T34882	hypothetical prote
187	6	1.4	119	2	T49306	hypothetical prote
188	6	1.4	120	2	T51675	myb-related transc
189	6	1.4	120	2	T44399	ribosomal protein
190	6	1.4	122	2	S29540	seminal vesicle se
191	6	1.4	122	2	G64946	lipoprotein yefP p
192	6	1.4	122	2	H81392	50S ribosomal prot
193	6	1.4	125	2	C24584	transposition regu
194	6	1.4	125	2	T31316	hypothetical prote
195	6	1.4	126	2	B75549	hypothetical prote
196	6	1.4	126	2	F72104	cytochrome P450 pr
197	6	1.4	127	2	PC2268	hypothetical 14.2k
198	6	1.4	127	2	E55098	cytochrome c' - Rh
199	6	1.4	128	1	CCRFX	cytochrome c' - Rh
200	6	1.4	128	1	K3H041	ig kappa chain pre
201	6	1.4	128	1	C83448	succinate dehydrog
202	6	1.4	129	1	CCRFP	cytochrome c' - Rh
203	6	1.4	129	1	OREBCY	chemotaxis protein
204	6	1.4	129	2	D70937	hypothetical prote
205	6	1.4	130	2	S75341	hypothetical prote
206	6	1.4	130	2	C69606	spore coat protein
207	6	1.4	131	2	G83088	hypothetical prote
208	6	1.4	133	2	H70657	hypothetical prote
209	6	1.4	133	2	T36525	hypothetical prote
210	6	1.4	134	2	A25748	lcb1 protein - Bac
211	6	1.4	134	2	A26986	hypothetical prote
212	6	1.4	137	2	T19799	hypothetical prote
213	6	1.4	139	2	C64844	probable membrane
214	6	1.4	139	2	B71280	hypothetical prote
215	6	1.4	142	1	F70437	conserved hypotet
216	6	1.4	142	2	T34862	nucleoside-diphosp
217	6	1.4	142	2	S16248	hypothetical prote
218	6	1.4	143	2	A17051	heat shock protein
219	6	1.4	143	2	S52834	hypothetical prote
220	6	1.4	145	2	A23971	hypothetical prote
221	6	1.4	146	2	F72458	probable gntR-fam1
222	6	1.4	146	2	T36436	conserved hypotet
223	6	1.4	148	2	B83525	hypothetical prote
224	6	1.4	148	2	S10655	hypothetical prote
225	6	1.4	148	2	S73004	hypothetical prote
226	6	1.4	149	2	F83483	conserved hypotet
227	6	1.4	149	2	J01541	hypothetical 16.9k
228	6	1.4	149	2	S48927	hypothetical prote
229	6	1.4	149	2	T37099	hypothetical prote
230	6	1.4	150	2	T01338	ribosomal protein
231	6	1.4	150	2	T47888	ribosomal protein
232	6	1.4	151	2	F75145	lsu ribosomal prot
233	6	1.4	151	2	B70862	hypothetical prote
234	6	1.4	151	2	T27900	hypothetical prote
235	6	1.4	151	2	A69786	hypothetical prote
236	6	1.4	151	2	T45983	hypothetical prote
237	6	1.4	152	2	S12629	heat shock cognate
238	6	1.4	154	2	T07625	heat shock protein
239	6	1.4	154	2	H69376	hypothetical prote
240	6	1.4	154	2	E70064	hypothetical prote
241	6	1.4	155	2	S50367	hypothetical prote
242	6	1.4	155	2	B28388	aminoglycoside 3''
243	6	1.4	156	2	J00351	heat shock protein
244	6	1.4	156	2	T49264	heat shock protein
245	6	1.4	156	2	S69594	heat shock protein
246	6	1.4	157	2	T14381	heat-shock protein
247	6	1.4	157	2	S16247	heat shock protein
248	6	1.4	158	2		

249	6	1.4	158	2	D81820	hypothetical prote	322	6	1.4	207	2	C81080	transglycosylase,
250	6	1.4	159	2	S72544	heat shock protein	323	6	1.4	209	2	JC4817	RNA-binding protei
251	6	1.4	159	2	T03958	heat shock protein	324	6	1.4	209	2	I40281	outer surface prot
252	6	1.4	159	2	H82723	conserved hypotet	325	6	1.4	210	2	A82740	transcription regu
253	6	1.4	159	2	A48428	homeotic protein H	326	6	1.4	210	2	E83471	probable transcrip
254	6	1.4	160	2	T10481	hypothetical 16.7k	327	6	1.4	210	2	T03865	hypothetical prote
255	6	1.4	160	2	E71942	hypothetical prote	328	6	1.4	211	1	S40836	formate dehydrogen
256	6	1.4	161	2	S00646	heat shock protein	329	6	1.4	211	2	H69539	SSU ribosomal prot
257	6	1.4	163	2	S62536	mannose-binding le	330	6	1.4	212	1	T04098	CBP20 preproprotei
258	6	1.4	163	2	S43762	mannose-binding le	331	6	1.4	212	1	WMBETA	23.5k protein - tu
259	6	1.4	163	2	S43764	mannose-binding le	332	6	1.4	212	2	D81929	probable indazole
260	6	1.4	163	2	T25838	hypothetical prote	333	6	1.4	212	2	A83199	probable transcrip
261	6	1.4	164	2	S32867	outw protein - Erw	334	6	1.4	213	2	B83182	probable two-compo
262	6	1.4	166	2	T03356	gene e1l protein -	335	6	1.4	213	2	I39581	nccn protein - Alc
263	6	1.4	166	2	S74330	hypothetical prote	336	6	1.4	214	2	T29397	hypothetical prote
264	6	1.4	168	2	I40352	single-stranded DN	337	6	1.4	215	2	G71800	ABC transporter, p
265	6	1.4	168	2	T35087	probable transcrip	338	6	1.4	215	2	A64717	ABC transporter, p
266	6	1.4	172	2	A46695	epididymal secreto	339	6	1.4	215	2	S74602	hypothetical prote
267	6	1.4	172	2	T10346	transcription repr	340	6	1.4	216	2	I38480	olfactory receptor
268	6	1.4	173	2	B39141	hypothetical prote	341	6	1.4	217	2	C75403	hypothetical prote
269	6	1.4	174	2	C72737	hypothetical prote	342	6	1.4	217	2	D69095	cobalamn biosynth
270	6	1.4	175	2	T46136	remorin-like prote	343	6	1.4	217	2	G70407	hypothetical prote
271	6	1.4	177	2	S53952	proteinase-2 precu	344	6	1.4	218	2	B49346	butyrate--acetace
272	6	1.4	177	2	T24466	hypothetical prote	345	6	1.4	218	2	F64806	ybgf protein - Esc
273	6	1.4	178	2	T44823	probable macrophag	346	6	1.4	219	2	A70734	probable cutinase
274	6	1.4	179	1	PWYBBB	H+-transporting At	347	6	1.4	219	2	S47773	hypothetical 22.2k
275	6	1.4	179	2	E36801	hypothetical prote	348	6	1.4	219	2	D70838	hypothetical prote
276	6	1.4	180	2	I48129	kel69 (escapes X-1	349	6	1.4	220	2	S74670	hypothetical prote
277	6	1.4	180	2	B83460	cytochrome C bioge	350	6	1.4	222	1	JL0085	eslinophil major b
278	6	1.4	180	2	T06718	hypothetical prote	351	6	1.4	223	2	B81991	NADH dehydrogenase
279	6	1.4	181	2	F70588	hypothetical prote	352	6	1.4	223	2	H81219	NADH dehydrogenase
280	6	1.4	181	2	T04827	SNF8 protein homol	353	6	1.4	224	2	B56111	propanediol dehydr
281	6	1.4	182	2	I59203	gene HOX2.8 protei	354	6	1.4	225	2	B72587	hypothetical prote
282	6	1.4	182	2	T30760	hypothetical prote	355	6	1.4	226	2	T51570	myb-related trans
283	6	1.4	184	2	D83462	conserved hypotet	356	6	1.4	227	2	H69845	hypothetical prote
284	6	1.4	185	2	T35471	ribosome recycling	357	6	1.4	228	2	E45170	cytochrome-c oxid
285	6	1.4	185	2	D75047	keto-valine-ferred	358	6	1.4	229	2	T06204	hypothetical prote
286	6	1.4	185	2	G71113	probable pyruvate	359	6	1.4	229	2	B41854	neutral proteinase
287	6	1.4	185	2	A48568	p28 antigen - Toxo	360	6	1.4	229	2	D72370	hypothetical prote
288	6	1.4	187	2	T50946	hypothetical prote	361	6	1.4	230	2	T21491	hypothetical prote
289	6	1.4	189	1	R7SP12	ribosomal protein	362	6	1.4	230	2	T51265	probable HLA DNA b
290	6	1.4	190	2	S50027	Ca2+-transporting	363	6	1.4	231	2	T38642	hypothetical prote
291	6	1.4	190	2	S70261	outer surface prot	364	6	1.4	232	2	J00886	hypothetical prote
292	6	1.4	190	2	F39741	hypothetical prote	365	6	1.4	233	1	JU0284	Fc gamma (19c) rec
293	6	1.4	191	2	B45164	hypothetical prote	366	6	1.4	233	2	B69753	conserved hypotet
294	6	1.4	191	2	A82613	conserved hypotet	367	6	1.4	235	2	S33448	transcription regu
295	6	1.4	192	2	B70352	hypothetical prote	368	6	1.4	237	2	S55614	hypothetical prote
296	6	1.4	194	1	MOCHLC	myosin alkali 11gh	369	6	1.4	237	2	G70612	hypothetical prote
297	6	1.4	194	1	S76403	hypothetical prote	370	6	1.4	238	1	I38016	melanoma-associate
298	6	1.4	194	2	F69102	thymidylate kinase	371	6	1.4	238	1	JC2297	CD63 antigen - rab
299	6	1.4	194	2	T10939	auxin-induced prot	372	6	1.4	238	1	A64963	conserved hypotet
300	6	1.4	195	1	MOHR3V	myosin alkali 11gh	373	6	1.4	238	2	T31218	hypothetical prote
301	6	1.4	195	2	A27241	helix-destabilizin	374	6	1.4	240	2	T19349	hypothetical prote
302	6	1.4	197	2	B83597	conserved hypotet	375	6	1.4	241	1	A64067	regulatory protein
303	6	1.4	199	2	B69340	cobalamn biosynth	376	6	1.4	241	2	C75329	conserved hypotet
304	6	1.4	199	1	S40810	hypothetical prote	377	6	1.4	242	2	H71219	hypothetical prote
305	6	1.4	200	1	MORR3V	myosin alkali 11gh	378	6	1.4	242	2	B64320	tRNA-pseudouridine
306	6	1.4	200	2	F81941	hypothetical prote	379	6	1.4	244	2	B83630	hypothetical prote
307	6	1.4	200	2	T09783	dehydration-induct	380	6	1.4	244	2	G81297	hypothetical prote
308	6	1.4	201	1	E69503	indolepyruvate fer	381	6	1.4	245	2	JQ1687	chalcone isomerase
309	6	1.4	201	2	F84043	hypothetical prote	382	6	1.4	246	2	T47651	chalcone isomerase
310	6	1.4	201	2	A75506	hypothetical prote	383	6	1.4	247	2	A57712	rod-core linker po
311	6	1.4	202	2	T08930	hypothetical prote	384	6	1.4	247	2	S23474	hypothetical cyto
312	6	1.4	202	2	A81441	probable orotate p	385	6	1.4	247	2	T50874	storage protein ho
313	6	1.4	203	2	F69381	flagellin (fla1-1	386	6	1.4	249	2	T06441	lipoprotein y1pA p
314	6	1.4	203	2	F83485	cob(1)alamn adeno	387	6	1.4	249	2	S14241	probable CObS - My
315	6	1.4	203	2	T35866	peptidyl integrat	388	6	1.4	249	2	A70786	conserved hypotet
316	6	1.4	205	2	F83075	peptidyl-prolyl cl	389	6	1.4	249	2	B83290	single chain Fv an
317	6	1.4	206	2	F70455	hypothetical prote	390	6	1.4	249	2	S41374	multicatalytic end
318	6	1.4	207	2	B46647	GTP-binding protei	391	6	1.4	252	1	SNBXS1	uridine phosphoryl
319	6	1.4	207	2	B36364	hypothetical prote	392	6	1.4	253	2	T46830	hypothetical prote
320	6	1.4	207	2	T38961	hypothetical prote	393	6	1.4	253	2	T02106	
321	6	1.4	207	2	F81862	probable transglyc	394	6	1.4	253	2		

395	6	1.4	253	2	G72598	probable ABC trans
396	6	1.4	254	1	JL0107	Fe gamma (IG) rec
397	6	1.4	254	1	UESY27	vegetative storage
398	6	1.4	254	2	T35366	probable membrane
399	6	1.4	254	2	T25073	hypothetical prote
400	6	1.4	255	1	S32482	electron transfer
401	6	1.4	255	2	S08625	hydrogenase (EC 1.
402	6	1.4	255	2	F71933	hypothetical prote
403	6	1.4	255	2	A71483	probable ABC trans
404	6	1.4	255	2	A24254	ecdysone-induced p
405	6	1.4	256	2	G83332	probable permease
406	6	1.4	256	2	D82201	spermidine/putresc
407	6	1.4	256	2	G83953	RNA polymerase sig
408	6	1.4	256	2	A34770	ORF1 protein - sal
409	6	1.4	257	1	D70893	enoyl-CoA hydratase
410	6	1.4	257	2	T50086	phosphomannomutase
411	6	1.4	257	2	E83050	probable transcrip
412	6	1.4	257	2	A27872	outer membrane pro
413	6	1.4	258	2	F81022	probable ABC trans
414	6	1.4	258	2	H82591	hydroxyacylglutath
415	6	1.4	259	2	A64509	tRNA-pseudouridine
416	6	1.4	259	2	T29459	hypothetical prote
417	6	1.4	259	2	A69476	conserved hypotet
418	6	1.4	259	2	T52619	conserved hypotet
419	6	1.4	260	2	S72748	TIMY-like protein
420	6	1.4	260	2	C82116	Bil17-F3_136 prote
421	6	1.4	261	2	G69099	flagellar biosynth
422	6	1.4	261	2	A83196	probable pyruvate
423	6	1.4	262	1	XUCSA	probable transcrip
424	6	1.4	262	2	C37392	streptomycin 3''-a
425	6	1.4	262	2	A25140	parasporel crystal
426	6	1.4	262	2	T02115	hypothetical prote
427	6	1.4	262	2	B64463	hypothetical prote
428	6	1.4	262	2	E83537	probable transcrip
429	6	1.4	263	2	JH0244	streptomycin/spect
430	6	1.4	263	2	J01756	streptomycin 3''-a
431	6	1.4	263	2	S05476	streptomycin 3''-a
432	6	1.4	263	2	C83616	beta-ketoadipate e
433	6	1.4	264	1	S35127	indole-3-glycerol-
434	6	1.4	264	1	CTMKP	coriolicropin / 11
435	6	1.4	264	2	G70075	amino acid ABC tra
436	6	1.4	264	2	C84028	sepium site-determ
437	6	1.4	264	2	T50659	alpha-expansin OSE
438	6	1.4	264	2	T36315	probable ABC-type
439	6	1.4	265	2	T20667	hypothetical prote
440	6	1.4	265	2	F83586	probable hydrolase
441	6	1.4	265	2	S19113	cycr-4 protein - C
442	6	1.4	266	2	I49114	Ly49H - mouse
443	6	1.4	267	2	F71679	cell division prot
444	6	1.4	267	2	C72415	zinc ABC transport
445	6	1.4	268	2	T46755	membrane protein a
446	6	1.4	269	2	T35068	indole-3-glycerol-
447	6	1.4	269	2	A70719	probable enoyl-CoA
448	6	1.4	269	2	T36001	probable integral
449	6	1.4	269	2	T49293	hypothetical prote
450	6	1.4	269	2	A49334	Ras homolog Rad -
451	6	1.4	270	1	S77085	molybdate-binding
452	6	1.4	270	2	E69379	chemotaxis protein
453	6	1.4	270	2	A34717	meiotic recombinat
454	6	1.4	270	2	C75283	hypothetical prote
455	6	1.4	271	2	T33688	probable methyltra
456	6	1.4	272	2	T23633	hypothetical prote
457	6	1.4	273	2	F69903	D-alanyl-D-alanine
458	6	1.4	273	2	S20069	ribonucleoprotein
459	6	1.4	274	2	E71257	conserved hypotet
460	6	1.4	274	2	G69460	conserved hypotet
461	6	1.4	275	1	E83412	streptomycin 3''-P
462	6	1.4	276	1	I39928	nitrate transport
463	6	1.4	276	1	A69077	conserved hypotet
464	6	1.4	276	1	D82648	hypothetical prote
465	6	1.4	277	1	ORECST	sulfate/thiosulfat
466	6	1.4	278	2	B75572	conserved hypotet
467	6	1.4	278	2	E83152	probable short-cha
468	6	1.4	279	2	S76873	hypothetical prote
469	6	1.4	279	2	JCA327	uridine phosphoryl
470	6	1.4	279	2	T19828	hypothetical prote
471	6	1.4	279	2	S26203	RNA-binding protei
472	6	1.4	279	2	I64215	hypothetical prote
473	6	1.4	280	2	T02090	xyloglucan endo-1,
474	6	1.4	280	2	S17717	RNA methylase - S
475	6	1.4	281	2	H72773	hypothetical prote
476	6	1.4	281	2	D72397	conserved hypotet
477	6	1.4	282	2	F72595	hypothetical prote
478	6	1.4	282	2	A75473	probable sigma fac
479	6	1.4	283	1	GJRT	gap junction prote
480	6	1.4	283	1	B49769	gap junction prote
481	6	1.4	283	1	B29005	gap junction prote
482	6	1.4	283	2	B56601	gap junction prote
483	6	1.4	283	2	H72087	comexin 32 - mous
484	6	1.4	284	2	G72363	hypothetical prote
485	6	1.4	284	2	T20237	cation efflux syst
486	6	1.4	285	2	T34836	hypothetical prote
487	6	1.4	286	2	T47064	probable dehydrata
488	6	1.4	286	2	B83259	hypothetical prote
489	6	1.4	286	2	S76153	hypothetical prote
490	6	1.4	286	2	T29719	hypothetical prote
491	6	1.4	287	2	C29674	phycocyanin linker
492	6	1.4	288	2	I48743	ryanodine receptor
493	6	1.4	288	2	T12462	hypothetical prote
494	6	1.4	289	2	T06565	acetyl-CoA carboxy
495	6	1.4	290	1	WMBEAK	38k phosphoprotein
496	6	1.4	290	1	WMBEIM	38k phosphoprotein
497	6	1.4	290	2	B69646	fructose-1,6-bisph
498	6	1.4	290	2	T03552	maltose transport
499	6	1.4	290	2	J00473	YnpA protein - Bac
500	6	1.4	291	1	CCPS2S	cytochrome c552 pr
501	6	1.4	291	2	S51608	RYB-a protein - ra
502	6	1.4	291	2	S46055	RYB-a protein - ra
503	6	1.4	291	2	C83504	conserved hypotet
504	6	1.4	292	2	T23966	hypothetical prote
505	6	1.4	292	2	S24169	hypothetical prote
506	6	1.4	293	2	E75431	mucin - rat
507	6	1.4	294	2	T08408	chorismate mutase/
508	6	1.4	294	2	A42594	transcription fact.
509	6	1.4	295	2	E75366	ORF1 5' to hyaA -
510	6	1.4	295	2	A56488	glutanyl-tRNA synt
511	6	1.4	296	2	T26723	Per8 peroxisomal i
512	6	1.4	296	2	A70973	hypothetical prote
513	6	1.4	296	2	E69025	hypothetical prote
514	6	1.4	297	2	I38517	conserved hypotet
515	6	1.4	297	2	S52726	syntaxin - human
516	6	1.4	297	2	T24718	syntaxin-4 - human
517	6	1.4	297	2	F69595	multidrug resistan
518	6	1.4	298	2	A49630	ubiquitin conjugat
519	6	1.4	298	2	T22390	hypothetical prote
520	6	1.4	298	2	S75205	hypothetical prote
521	6	1.4	298	2	C81516	hypothetical prote
522	6	1.4	298	2	G72582	hypothetical prote
523	6	1.4	298	2	T31236	protein disulfide-
524	6	1.4	299	2	D81067	hypothetical prote
525	6	1.4	299	2	B83161	hypothetical prote
526	6	1.4	300	2	F75586	urea/short-chain a
527	6	1.4	301	2	S62199	formylmethanofuran
528	6	1.4	301	2	G83344	probable permease
529	6	1.4	302	1	PAFFIA	phosphoprotein pho
530	6	1.4	302	2	S29386	phosphoprotein pho
531	6	1.4	302	2	T51905	hypothetical prote
532	6	1.4	302	2	T19348	hypothetical prote
533	6	1.4	302	2	T21843	hypothetical prote
534	6	1.4	303	2	S37546	H+-transporting AT
535	6	1.4	303	2	A71102	hypothetical prote
536	6	1.4	304	1	S74557	acetylpolylamine am
537	6	1.4	304	2	A32993	transcription fact
538	6	1.4	304	2	H81349	probable periplasm
539	6	1.4	305	2	T28005	hypothetical prote
540	6	1.4	305	2	H83344	hypothetical prote

541	6	1.4	306	2	T06042	hypothetical prote	614	6	1.4	338	2	F83965	molYbdppterln cofa
542	6	1.4	307	2	B75120	phosphoglycerate d	615	6	1.4	339	2	A53066	CCAAT enhancer-bin
543	6	1.4	307	2	E71011	probable phosphogl	616	6	1.4	338	1	TVRRM	protein kinase (EC
544	6	1.4	307	2	B81196	agmatinase (EC 3.5	617	6	1.4	339	2	T25204	hypothetical prote
545	6	1.4	307	2	B36125	branched-chain aml	618	6	1.4	340	1	Q0BES6	lipopolysaccharide
546	6	1.4	307	2	C70734	hypothetical prote	619	6	1.4	340	2	G64554	lipopolysaccharide
547	6	1.4	308	2	H64409	hypothetical prote	620	6	1.4	340	2	A64902	peptide transport
548	6	1.4	309	1	A57235	RING finger protei	621	6	1.4	340	2	T44930	mocp protein (limpo
549	6	1.4	309	2	T00503	myb-related protei	622	6	1.4	340	2	A72600	probable dehydroge
550	6	1.4	309	2	T08150	chitinase (EC 3.2.	623	6	1.4	341	1	D69664	molYbdppterln cofa
551	6	1.4	310	2	A75312	branched-chain aml	624	6	1.4	341	1	T40858	translation Initia
552	6	1.4	311	2	H75411	conserved hypotnet	625	6	1.4	342	1	TVWMV9	protein kinase (EC
553	6	1.4	312	2	T23521	hypothetical prote	626	6	1.4	342	2	T08474	Kfira protein - Ent
554	6	1.4	312	2	H83245	hypothetical prote	627	6	1.4	344	2	D72116	hypothetical prote
555	6	1.4	313	2	E70871	hypothetical prote	628	6	1.4	344	2	A64103	DMN-directed DNA p
556	6	1.4	313	2	H71438	hypothetical prote	629	6	1.4	345	2	S12788	transcription fact
557	6	1.4	314	1	G64658	probable pyruvate	630	6	1.4	345	2	A58519	hypothetical 345 p
558	6	1.4	314	1	A71858	pyruvate ferrodoxl	631	6	1.4	346	2	T25212	hypothetical prote
559	6	1.4	315	2	S74357	hypothetical prote	632	6	1.4	346	2	A81554	hypothetical prote
560	6	1.4	315	2	T46156	hypothetical prote	633	6	1.4	346	2	S55491	probable galactosy
561	6	1.4	316	1	J00956	myb-related protei	634	6	1.4	346	2	S41001	hypothetical prote
562	6	1.4	317	2	T12055	melanocyte stimula	635	6	1.4	347	1	MNMRWE	nonstructural prot
563	6	1.4	317	2	S45708	MSH receptor - bov	636	6	1.4	347	1	S69719	hypothetical prote
564	6	1.4	318	2	D82742	dihydroxydipicolin	637	6	1.4	348	2	C64676	oligopeptide ABC t
565	6	1.4	318	2	A69992	conserved hypotnet	638	6	1.4	348	2	C71841	probable peptide A
566	6	1.4	318	2	T35367	hypothetical prote	639	6	1.4	348	2	S34244	43K structural pro
567	6	1.4	318	2	T43492	hypothetical prote	640	6	1.4	351	2	B49906	rfib homolog - Xan
568	6	1.4	319	2	B71312	probable GTP-bindl	641	6	1.4	351	2	C81892	sulfate ABC transp
569	6	1.4	319	2	T35337	probable ion chann	642	6	1.4	351	2	A81132	sulfate ABC transp
570	6	1.4	320	1	DDRT	heliX-deStabilizin	643	6	1.4	351	2	S73356	hypothetical prote
571	6	1.4	320	1	A44485	heterogeneous ribo	644	6	1.4	351	2	S58192	hypothetical prote
572	6	1.4	320	2	S02061	heterogeneous ribo	645	6	1.4	351	2	S40840	hypothetical 39.3K
573	6	1.4	320	2	S30192	heterogeneous ribo	646	6	1.4	351	2	E81785	transaldolase (EC
574	6	1.4	320	2	S04617	heterogeneous ribo	647	6	1.4	351	2	E81210	transaldolase NMB0
575	6	1.4	320	2	T16358	hypothetical prote	648	6	1.4	352	2	T10956	naringenin-chalcon
576	6	1.4	320	2	E75255	hypothetical prote	649	6	1.4	352	2	S44853	K12H4.3 protein -
577	6	1.4	321	1	D69112	2-phosphoglycerate	650	6	1.4	353	2	S71338	t-complex protein
578	6	1.4	321	2	S30606	senescence-related	651	6	1.4	354	2	D35255	probable trans-chn
579	6	1.4	321	2	D70070	transcription regu	652	6	1.4	355	2	T80169	class I histocompa
580	6	1.4	321	2	T43194	hypothetical prote	653	6	1.4	356	1	S03320	regulatory protein
581	6	1.4	322	2	E69009	catlon antiporter	654	6	1.4	356	2	B71910	Integrase-recombin
582	6	1.4	322	2	S63258	ribosomal protein	655	6	1.4	356	2	T51376	Integrase-recombin
583	6	1.4	323	2	I40986	streptomycin/spect	656	6	1.4	357	2	B72405	conserved hypotnet
584	6	1.4	323	2	T15808	hypothetical prote	657	6	1.4	359	1	A64598	protein E - Helico
585	6	1.4	325	1	S46438	cysteine synthase	658	6	1.4	359	2	S33317	homoserine dehydro
586	6	1.4	325	2	S35094	cysteine synthase	659	6	1.4	359	2	T50704	replication factor
587	6	1.4	325	2	A40963	phospholipase A2-a	660	6	1.4	359	2	E71914	hypothetical prote
588	6	1.4	326	2	H70622	hypothetical prote	661	6	1.4	360	2	C70185	carotenoid biosynt
589	6	1.4	326	2	T07711	hypothetical prote	662	6	1.4	361	2	S56488	hypothetical 39.8K
590	6	1.4	327	2	S13827	phosphoprotein pho	663	6	1.4	361	2	T45918	hypothetical prote
591	6	1.4	327	2	T09687	chitinase (EC 3.2.	664	6	1.4	361	2	T00437	probable protein d
592	6	1.4	327	2	T01038	myb-related protei	665	6	1.4	362	2	C64604	Integrase/recombin
593	6	1.4	327	2	T34996	probable transcrip	666	6	1.4	362	2	T52038	probable pnytochel
594	6	1.4	328	2	F84130	ABC transporter (p	667	6	1.4	362	2	T45072	erythroid Kruppel-
595	6	1.4	328	2	G70357	flagellar switch p	668	6	1.4	363	2	B83436	chiasmata syntphas
596	6	1.4	329	2	S28442	exb protein - Pse	669	6	1.4	363	2	S07113	class I histocompa
597	6	1.4	329	2	B75615	pyridoxamine kinas	670	6	1.4	363	2	S75088	probable GTP-bindl
598	6	1.4	330	2	C64792	ferric enterobacti	671	6	1.4	363	2	B65057	hypothetical prote
599	6	1.4	330	2	F64905	probable sugar tra	672	6	1.4	364	2	T01184	hypothetical prote
600	6	1.4	332	2	T35830	acetylactate synth	673	6	1.4	365	2	E82585	histidinol-phospha
601	6	1.4	332	2	T15561	G protein-coupled	674	6	1.4	365	2	I68896	nonclassical class
602	6	1.4	332	2	A83428	hypothetical prote	675	6	1.4	365	2	P00839	envelope protein -
603	6	1.4	333	2	T45720	probable transcrip	676	6	1.4	365	2	P00838	envelope protein -
604	6	1.4	333	2	S75754	hypothetical prote	677	6	1.4	365	2	P00840	envelope protein -
605	6	1.4	333	2	E81748	glutamyl-tRNA redu	678	6	1.4	365	2	C83885	hypothetical prote
606	6	1.4	335	2	E71215	hypothetical prote	679	6	1.4	365	2	F84033	germination (corfe
607	6	1.4	335	2	G82224	probable vitamin B	680	6	1.4	366	2	E69375	ABC transporter, A
608	6	1.4	335	2	T50600	secreted acetylXyl	681	6	1.4	366	2	A55525	carboxy-cis,cis-mu
609	6	1.4	335	2	S42807	HSR03J protein -	682	6	1.4	367	2	T29752	hypothetical prote
610	6	1.4	336	2	G71954	lipopolysaccharide	683	6	1.4	367	2	JE0349	interferon-inducib
611	6	1.4	337	2	C83370	conserved hypotnet	684	6	1.4	367	2	E64399	hypothetical prote
612	6	1.4	337	2	S06956	segmentation prote	685	6	1.4	368	2	T36029	probable transcrip
613	6	1.4	338	2	E83059	ketol-acid reducto	686	6	1.4	368	2	A53439	RP protein - human

687	6	1.4	369	2	S77199	760	6	1.4	399	2	C83611	hypothetical prote
688	6	1.4	369	2	G72069	761	6	1.4	400	2	I50219	connexin 45.6 - ch
689	6	1.4	369	2	H70650	762	6	1.4	400	2	S43376	calreticulin, brai
690	6	1.4	369	2	T29120	763	6	1.4	401	2	A63368	hypothetical prote
691	6	1.4	369	2	T46299	764	6	1.4	401	2	T39310	hypothetical prote
692	6	1.4	370	1	A69396	765	6	1.4	402	2	B82491	Nupc family protei
693	6	1.4	370	2	A72573	766	6	1.4	402	2	S61413	DNA-binding protei
694	6	1.4	370	2	T47131	767	6	1.4	403	2	S03960	S-antigen - rat
695	6	1.4	371	2	C70337	768	6	1.4	403	2	I50066	S-antigen - mouse
696	6	1.4	371	2	T49908	769	6	1.4	403	2	H70931	probable PPE prote
697	6	1.4	371	2	T30762	770	6	1.4	403	2	G64427	hypothetical prote
698	6	1.4	374	1	TVWVHT	771	6	1.4	404	1	S77553	probable hexosyltr
699	6	1.4	374	2	A83483	772	6	1.4	404	1	LABECA	latent membrane pr
700	6	1.4	375	2	S63685	773	6	1.4	404	2	G69318	threonine synthase
701	6	1.4	375	2	T36889	774	6	1.4	404	2	G75161	membrane lipoprote
702	6	1.4	375	2	T43850	775	6	1.4	405	2	A25379	saccharopepsin (EC
703	6	1.4	375	2	T43852	776	6	1.4	405	2	A60534	p2b/LAMP-1-precurs
704	6	1.4	376	1	TVWVIM	777	6	1.4	405	2	S46828	probable GTP-bindi
705	6	1.4	376	1	A48681	778	6	1.4	405	2	T27971	hypothetical prote
706	6	1.4	376	2	S27015	779	6	1.4	405	2	A28009	43k postsynaptic m
707	6	1.4	376	2	A82745	780	6	1.4	405	2	H82632	ATPase xrl828 [imp
708	6	1.4	377	2	T04213	781	6	1.4	405	2	T48534	hypothetical prote
709	6	1.4	378	2	A33973	782	6	1.4	406	2	A83104	probable hydrolase
710	6	1.4	378	2	T24254	783	6	1.4	406	2	S40774	conserved hypotbet
711	6	1.4	378	2	G75446	784	6	1.4	406	2	H69812	conserved hypotbet
712	6	1.4	378	2	A44443	785	6	1.4	407	1	A55515	tyrosine--tRNA lig
713	6	1.4	379	2	S13556	786	6	1.4	407	2	H72573	probable acetyl Co
714	6	1.4	379	2	F72022	787	6	1.4	407	2	A72691	probable spermidin
715	6	1.4	380	2	JCS747	788	6	1.4	407	2	S76946	hypothetical prote
716	6	1.4	380	2	T16883	789	6	1.4	409	2	D70354	theonine synthase
717	6	1.4	380	2	A49778	790	6	1.4	409	2	E69433	conserved hypotbet
718	6	1.4	381	2	S34848	791	6	1.4	410	2	D75037	hypothetical prote
719	6	1.4	381	2	S37297	792	6	1.4	411	2	C71660	tyrosine--tRNA lig
720	6	1.4	381	2	T24256	793	6	1.4	411	2	S61245	probable vitron g1
721	6	1.4	381	2	S16506	794	6	1.4	411	2	T35102	probable transmemb
722	6	1.4	381	2	S60561	795	6	1.4	411	2	S41945	hypothetical prote
723	6	1.4	382	2	I39780	796	6	1.4	412	2	A83461	hypothetical prote
724	6	1.4	382	2	I39068	797	6	1.4	412	2	T48405	myb-like protein -
725	6	1.4	382	2	A47477	798	6	1.4	413	2	D72388	hypothetical prote
726	6	1.4	383	2	G75431	799	6	1.4	413	2	S70401	zona pellucida gly
727	6	1.4	384	2	S60212	800	6	1.4	415	2	G72335	hypothetical prote
728	6	1.4	386	2	S53965	801	6	1.4	415	1	S06763	calreticulin precu
729	6	1.4	387	1	A43704	802	6	1.4	416	2	JH0819	calreticulin precu
730	6	1.4	387	2	I50703	803	6	1.4	417	1	A37047	calreticulin precu
731	6	1.4	387	2	D70090	804	6	1.4	417	2	H81340	probable proteinas
732	6	1.4	387	2	D82134	805	6	1.4	417	2	S10871	phosphotransferas
733	6	1.4	387	2	T50675	806	6	1.4	417	2	JH0660	amine dehydrogenas
734	6	1.4	388	2	E81244	807	6	1.4	417	2	T01616	hypothetical prote
735	6	1.4	388	2	D82023	808	6	1.4	417	2	T18769	hypothetical prote
736	6	1.4	389	2	T03612	809	6	1.4	418	1	A34154	hypothetical prote
737	6	1.4	389	2	T02970	810	6	1.4	418	1	E75587	calreticulin precu
738	6	1.4	389	2	S36638	811	6	1.4	419	2	S69207	probable glycosylt
739	6	1.4	389	2	C82637	812	6	1.4	420	1	E82856	vascular endotheli
740	6	1.4	391	2	C72220	813	6	1.4	420	1	EFHST	conserved hypotbet
741	6	1.4	392	2	A84125	814	6	1.4	421	2	T09379	translaton elonga
742	6	1.4	392	2	T44362	815	6	1.4	422	2	S58173	probable translati
743	6	1.4	392	2	T38881	816	6	1.4	422	2	A83473	ketocacyl synthase
744	6	1.4	392	2	F72632	817	6	1.4	422	1	A83473	3-oxoacyl-acyl car
745	6	1.4	393	1	C56274	818	6	1.4	423	1	VHWVSB	structural polypro
746	6	1.4	394	2	DV1379	819	6	1.4	423	1	MRBY	mRNA maturase b13
747	6	1.4	395	2	A47701	820	6	1.4	423	2	S78662	mRNA maturase SCBI
748	6	1.4	396	2	D69378	821	6	1.4	423	2	H70501	hypothetical prote
749	6	1.4	396	2	T10958	822	6	1.4	424	2	T05785	probable tyrs prot
750	6	1.4	396	2	T10999	823	6	1.4	424	2	S53004	hypothetical prote
751	6	1.4	396	2	T09618	824	6	1.4	425	2	E719484	mitosis-specific c
752	6	1.4	396	2	T11000	825	6	1.4	425	2	A64625	hypothetical prote
753	6	1.4	396	2	T10960	826	6	1.4	426	2	E71889	pantothenate metab
754	6	1.4	396	2	A34401	827	6	1.4	426	2	A82660	glucose/galactose
755	6	1.4	396	2	S62008	828	6	1.4	426	2	T35550	probable transmemb
756	6	1.4	397	1	XNMCY	829	6	1.4	426	2	F82315	conserved hypotbet
757	6	1.4	397	1	DCNCP	830	6	1.4	426	2	E71408	probable acylamino
758	6	1.4	397	1	E69295	831	6	1.4	427	2	T50906	protecholeophyllid
759	6	1.4	397	2	E69858	832	6	1.4	427	2	JA0073	genome polyprotein

833	6	1.4	428	2	E71336	probable glutamate
834	6	1.4	428	2	G71023	translation elonga
835	6	1.4	428	2	C75110	translation elonga
836	6	1.4	428	2	D70583	probable transmem
837	6	1.4	428	2	S65585	probable NAD(P)-de
838	6	1.4	428	2	G56273	protein-histidine
839	6	1.4	429	2	S72829	trehalose-6-phosph
840	6	1.4	430	2	S19000	translation elonga
841	6	1.4	430	2	E82557	ABC transporter su
842	6	1.4	431	2	H70731	probable esterase
843	6	1.4	431	2	S20065	nuclear factor I-X
844	6	1.4	432	2	S26697	aprt protein - pse
845	6	1.4	432	2	S20108	nuclear protein -
846	6	1.4	432	2	A70714	hypothetical prote
847	6	1.4	432	2	G83489	alkaline proteinas
848	6	1.4	433	1	JN0560	u-plasminogen acti
849	6	1.4	433	2	B71568	hypothetical prote
850	6	1.4	433	2	G83042	hypothetical prote
851	6	1.4	433	2	B47041	hypothetical prote
852	6	1.4	434	2	B72328	conserved hypothet
853	6	1.4	435	1	S65982	transport protein
854	6	1.4	435	2	S27453	meiotic recombinat
855	6	1.4	435	2	S75346	hypothetical prote
856	6	1.4	435	2	F71444	probable carboxyl-
857	6	1.4	435	2	T34200	hypothetical prote
858	6	1.4	436	2	S76539	exopolysaccharide
859	6	1.4	436	2	T05653	amino acid transpo
860	6	1.4	438	2	B83295	hypothetical prote
861	6	1.4	438	2	I38946	melanoma ubiquitin
862	6	1.4	440	2	T31458	protochlorophyllid
863	6	1.4	440	2	D83805	hypothetical prote
864	6	1.4	441	2	T22531	hypothetical prote
865	6	1.4	441	2	A48959	glutamate-1-semial
866	6	1.4	442	2	T14353	probable 4-hydroxy
867	6	1.4	442	2	A83211	conserved hypothet
868	6	1.4	442	2	D64995	hypothetical prote
869	6	1.4	442	2	JC6594	jerky gene protein
870	6	1.4	443	2	B81122	phage virion prote
871	6	1.4	444	2	S51199	tryptophan 5-monoo
872	6	1.4	444	2	T19855	hypothetical prote
873	6	1.4	444	2	A72209	hypothetical prote
874	6	1.4	445	2	D83819	hypothetical prote
875	6	1.4	446	2	D82730	adenosylhomocystei
876	6	1.4	446	2	S56352	dicarboxylate tran
877	6	1.4	446	2	G75304	conserved hypothet
878	6	1.4	447	2	S17434	translation elonga
879	6	1.4	447	2	S53982	hypothetical prote
880	6	1.4	447	2	B82490	probable Na+/H+ an
881	6	1.4	447	2	T50705	gamma-aminobutyrat
882	6	1.4	448	2	B82171	probable sodium-de
883	6	1.4	448	2	T06698	hypothetical prote
884	6	1.4	449	2	F81954	ubiquitin--cytochr
885	6	1.4	449	2	E81011	ubiquitin--cytochr
886	6	1.4	449	2	S21989	translation elonga
887	6	1.4	449	2	T02625	hypothetical prote
888	6	1.4	450	2	B71304	probable zinc prot
889	6	1.4	450	2	A44751	carotenoid-binding
890	6	1.4	450	2	T37702	hypothetical prote
891	6	1.4	450	2	T23111	hypothetical prote
892	6	1.4	452	2	A64933	celb protein - Esc
893	6	1.4	453	2	D84018	two-component resp
894	6	1.4	453	2	E83517	conserved hypothet
895	6	1.4	453	2	T15374	hypothetical prote
896	6	1.4	454	2	T20829	probable serine ca
897	6	1.4	455	2	B71480	probable agx-1 hom
898	6	1.4	455	2	S76009	hypothetical prote
899	6	1.4	457	2	I51660	dopamine D1B recep
900	6	1.4	457	2	J01413	hypothetical 50.9k
901	6	1.4	458	2	A26940	nitrogenase molybd
902	6	1.4	458	2	B81325	probable C4-dicarb
903	6	1.4	458	2	D70410	cytosolic axial fil
904	6	1.4	460	2	H83264	probable transport
905	6	1.4	461	2	B64992	acetoacetate metab
906	6	1.4	461	2	G83602	hypothetical prote
907	6	1.4	461	2	T03561	hypothetical prote
908	6	1.4	461	2	T36599	probable beta-lact
909	6	1.4	462	1	EPSS1A	translation elonga
910	6	1.4	462	2	S50143	translation elonga
911	6	1.4	463	2	T26655	hypothetical prote
912	6	1.4	464	2	I37227	cyclin-dependent k
913	6	1.4	464	2	T15161	hypothetical prote
914	6	1.4	465	2	T16618	hypothetical prote
915	6	1.4	465	2	F83320	sirochrome synthase
916	6	1.4	466	2	T09356	hypothetical prote
917	6	1.4	466	2	T08914	hypothetical prote
918	6	1.4	466	2	A37351	IMP-E2 protein pre
919	6	1.4	467	2	S75150	glutamate decarbox
920	6	1.4	467	2	S62591	translation initia
921	6	1.4	467	2	A82564	conserved hypothet
922	6	1.4	467	2	T16319	hypothetical prote
923	6	1.4	468	2	S52495	acid phosphatase h
924	6	1.4	468	2	D69716	involved in spore
925	6	1.4	468	2	D70557	probable lgt prote
926	6	1.4	470	2	H82054	conserved hypothet
927	6	1.4	471	2	T49019	probable RNA bindi
928	6	1.4	472	2	F82639	resistance protein
929	6	1.4	472	2	H70873	probable exported
930	6	1.4	475	2	B37761	ntra protein - Thi
931	6	1.4	476	2	A83387	probable transport
932	6	1.4	477	1	ORH0B1	beta-1-adrenergic
933	6	1.4	477	2	A49937	50k outer membrane
934	6	1.4	478	2	G83048	probable two-compo
935	6	1.4	478	2	S31906	beta-1,3-glucanase
936	6	1.4	478	2	JC7326	blood P02 containin
937	6	1.4	479	2	F70680	probable obg - Myc
938	6	1.4	480	1	A45614	meroxite surface
939	6	1.4	480	2	I53053	beta 1 adrenergic
940	6	1.4	480	2	D43561	metazollite surface
941	6	1.4	481	2	S69808	lincomycin resista
942	6	1.4	481	2	F83363	probable AGCS sodi
943	6	1.4	481	2	A64941	hypothetical prote
944	6	1.4	481	2	A69276	conserved hypothet
945	6	1.4	482	2	T39455	adenylosuccinate 1
946	6	1.4	482	2	T02355	hypothetical prote
947	6	1.4	482	2	G83490	probable outer mem
948	6	1.4	482	2	T44628	probable transposa
949	6	1.4	482	2	A70963	hypothetical prote
950	6	1.4	483	2	S16531	xylokinase (EC 2
951	6	1.4	483	2	B71537	probable n-acetylm
952	6	1.4	483	2	F75360	hypothetical prote
953	6	1.4	484	2	F71061	hypothetical prote
954	6	1.4	484	2	F83593	outer membrane pro
955	6	1.4	485	2	A82414	probable chitinase
956	6	1.4	485	2	S52411	ZNF165 protein - h
957	6	1.4	486	2	S47891	exuperantile protel
958	6	1.4	486	2	T33445	probable integral
959	6	1.4	487	2	C70830	probable PPE prote
960	6	1.4	487	2	D71497	hypothetical prote
961	6	1.4	488	2	C83533	succinylglutamate
962	6	1.4	489	1	H70729	cytochrome P450 Rv
963	6	1.4	489	2	T27445	hypothetical prote
964	6	1.4	490	2	T23112	hypothetical prote
965	6	1.4	491	2	F81655	conserved hypothet
966	6	1.4	492	2	E75595	conserved hypothet
967	6	1.4	493	2	H70573	hypothetical prote
968	6	1.4	495	2	T18835	hypothetical prote
969	6	1.4	496	2	C83617	probable aldehyde
970	6	1.4	496	2	A37979	cartilage matrix p
971	6	1.4	496	2	S61716	ribose-phosphate p
972	6	1.4	497	2	F82747	conserved hypothet
973	6	1.4	498	1	JQ0197	4-aminobutyrate tr
974	6	1.4	498	2	A70630	probable lpgm prot
975	6	1.4	499	2	T49064	cytochrome P450-11
976	6	1.4	499	2	S74045	glycerol kinase (E
977	6	1.4	499	2	I51257	retinoic acid rece
978	6	1.4	500	2	T50868	exopolysphatase

979 6 1.4 501 2 F71965 lysine--tRNA ligas
 980 6 1.4 501 2 F64542 lysine--tRNA ligas
 981 6 1.4 501 2 S18573 L-lysine transport
 982 6 1.4 502 2 T35743 ribosomal protein
 983 6 1.4 502 2 B70845 probable sygar tra
 984 6 1.4 502 2 T01179 hypothetical prote
 985 6 1.4 503 2 T24985 hypothetical prote
 986 6 1.4 503 2 T34694 probable cationic
 987 6 1.4 503 2 S77290 hypothetical prote
 988 6 1.4 504 2 S46752 conserved hypothet
 989 6 1.4 504 2 T43496 hypothetical prote
 990 6 1.4 504 2 F72744 hypothetical prote
 991 6 1.4 504 2 A83901 hypothetical prote
 992 6 1.4 505 2 C46642 DNA primase (EC 2.
 993 6 1.4 505 2 C46642 phosphotransferase
 994 6 1.4 506 1 M0EC2S hypothetical prote
 995 6 1.4 507 2 T00871 probable DNA repair
 996 6 1.4 507 2 A81413 aspartic proteinas
 997 6 1.4 508 2 S19697 glucose-6-phosphat
 998 6 1.4 509 2 S77348 probable beta-fruc
 999 6 1.4 509 2 T06226 nucleoprotein - S1
 1000 6 1.4 509 2 J01269

ALIGNMENTS

RESULT 1

T03653
 phospholipid transfer protein homolog - maize (fragment)
 N:Alternate names: hypothetical protein O
 C:Species: Zea mays (maize)
 C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 16-Jul-1999
 C:Accession: T03653
 R:Keith, C.S.; Hoang, D.O.; Barrett, B.M.; Feigelman, B.; Nelson, M.C.; Thai, H.; Baysdo
 Plant Physiol. 101, 329-332, 1993
 A:Title: Partial sequence analysis of 130 randomly selected maize cDNA clones.
 A:Reference number: Z14989; MUID:94105294
 A:Accession: T03653
 A:Molecule type: mRNA
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Residues: 1-29 <KEI>
 A:Cross-references: EMBL:M95074; NID:g168563; PIDN:AAA18561.1; PID:g168564
 C:Superfamily: phospholipid transfer protein

Query Match 1.8%; Score 8; DB 2; Length 29;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 VVAVALLL 48
 DB 12 VVAVALLL 19

RESULT 2

T04093
 phospholipid transfer protein - maize
 C:Species: Zea mays (maize)
 C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 16-Jul-1999
 C:Accession: T04093
 R:Betawar, N.M.; Hoang, D.; Baysdorfer, C.
 Submitted to the EMBL Data Library, August 1996
 A:Reference number: Z15204
 A:Accession: T04093
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-121 <BEI>
 A:Cross-references: EMBL:U66105; NID:g1498596; PIDN:AAB06443.1; PID:g1498597
 A:Experimental source: strain B73
 C:Superfamily: phospholipid transfer protein
 C:Keywords: lipid transport

Query Match 1.8%; Score 8; DB 2; Length 121;
 Best Local Similarity 100.0%; Pred. No. 3.9;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 VVAVALLL 48
 DB 12 VVAVALLL 19

RESULT 3

T51712
 threonine dehydratase/deaminase [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 17-Nov-2000
 C:Accession: T51712
 R:Mourat, G.S.; Emerick, R.M.; Marion, A.L.; Smith, A.M.
 submitted to the EMBL Data Library, October 1998
 A:Reference number: Z25433
 A:Accession: T51712
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-592 <MOU>
 A:Cross-references: EMBL:AF096281; PIDN:AAC97936.1
 C:Genetics:
 A:Gene: OMRI
 C:Superfamily: threonine dehydratase

Query Match 1.8%; Score 8; DB 2; Length 592;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 283 QYPEQEME 290
 DB 558 QYPEQEME 565

RESULT 4

D71391
 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - common lancelet mitochondrion
 C:Species: mitochondrion Branchiostoma lanceolatum (common lancelet)
 C:Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 20-Jun-2000
 C:Accession: D71391
 R:Spruyt, N.; Delarbre, C.; Gachelin, G.; Laudet, V.
 Nucleic Acids Res. 26, 3279-3285, 1998
 A:Title: Complete sequence of the amphioxus (Branchiostoma lanceolatum) mitochondrial
 A:Reference number: A71390; MUID:98292550
 A:Accession: D71391
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-598 <SPR>
 A:Cross-references: GB:Y16474; NID:g3292989; PIDN:CAA76257.1; PID:g3293001
 C:Genetics:
 A:Gene: NADH5
 A:Genome: mitochondrion
 A:Genetic code: SGC4
 C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5
 C:Keywords: membrane associated complex; mitochondrion; NAD; oxidative phosphorylation

Query Match 1.8%; Score 8; DB 2; Length 598;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 LLLVSAES 53
 DB 122 LLLVSAES 129

RESULT 5

Q00BET0
 B0LF1 protein - human herpesvirus 4 (strain B95-8)

C:Species: human herpesvirus 4, Epstein-Barr virus
 C>Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 16-Jul-1999
 C:Accession: A43041; A03752; S32995
 R:Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barrell, B.G.
 M.Ol. Biol. Med. 1, 21-45, 1983
 A>Title: Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8 Epstein-Barr virus
 A:Reference number: A93065; MID:85035713
 A:Accession: A43041
 A:Molecule type: DNA
 A:Residues: 1-1239 <BAM>
 A:Cross-references: EMBL:V01555; NID:g59074; PIDN:CAA24844.1; PID:g1334855
 R:Baer, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.; H
 Nature 310, 207-211, 1984
 A>Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome.
 A:Reference number: A03794; MID:84270667
 A:Contents: annotation; protein coding region
 C:Superfamily: human herpesvirus 4 BOLF1 protein

Query Match 1.6%; Score 7; DB 1; Length 1239;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 322 RRLVPA 329
 |||||
 DB 874 RRLVPA 881

RESULT 6
 S44288
 rex protein - simian immunodeficiency virus SIVag (fragment)
 C:Species: simian immunodeficiency virus SIVag
 C>Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 08-Oct-1999
 C:Accession: S44288
 R:Vandamme, A.M.
 submitted to the EMBL Data Library, May 1994
 A:Reference number: S44288
 A:Accession: S44288
 A:Molecule type: DNA
 A:Residues: 1-39 <VAN>
 A:Cross-references: EMBL:232851; NID:g483445; PIDN:CAA83685.1; PID:g483447
 A:Experimental source: cell-line PB 1664
 A:Note: the source is designated as primate T-cell lymphotropic virus

Query Match 1.6%; Score 7; DB 2; Length 39;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 199 TSSPGTP 205
 |||||
 DB 33 TSSPGTP 39

RESULT 7
 AKIOL2
 adipokine hormone II precursor - migratory locust
 N:Alternate names: adipokine hormone II precursor-related peptide; Lom-AKH-II; peptid
 N:Contains: adipokine hormone II; adipokine hormone-associated peptide II
 C:Species: Locusta migratoria (migratory locust)
 C>Date: 31-Mar-1988 #sequence_revision 07-Nov-1997 #text_change 16-Jun-2000
 C:Accession: B58652; B25204; B24241; B58653
 R:Boiger, J.; Koolman, F.P.; Pijnenburg, M.A.P.; Hekling, L.H.P.; Oudejans, R.C.H.M.; Va
 J. Biol. Chem. 270, 23038-23043, 1995
 A>Title: Molecular cloning of three distinct cDNAs, each encoding a different adipokine
 okine hormone precursor genes during flight activity.
 A:Reference number: A58652; MID:96032738
 A:Accession: B58652
 A:Molecule type: mRNA
 A:Residues: 1-61 <BOG>
 A:Cross-references: GB:X86800; NID:g1085062; PIDN:CAA60495.1; PID:g1085063
 R:Siegel, K.; Morgan, P.; Mordue, W.
 Biol. Chem. Hoppe-Seyler 366, 723-727, 1985

A>Title: Primary structures of locust adipokine hormones II.
 A:Reference number: A90692; MID:86050918
 A:Accession: B25204

A:Molecule type: protein
 A:Residues: 23-30 <SIE>
 R:Gade, G.; Goldsworthy, G.J.; Schaffer, M.H.; Cook, J.C.; Rinehart Jr., K.L.
 Biochem. Biophys. Res. Commun. 134, 723-730, 1986
 A>Title: Sequence analyses of adipokine hormones II from corpora cardiaca of Schis
 A:Reference number: A24241; MID:86130555
 A:Accession: B24241

A:Molecule type: protein
 A:Residues: E, 24-30 <GAD>
 R:Heiter, H.; Luu, B.; Goltzene, F.; Zachary, D.; Hoffmann, J.; Van Dorsselaer, A.
 Eur. J. Biochem. 182, 77-84, 1989
 A>Title: Isolation and structure of two novel 6-kDa dimeric peptides from the corpora
 A:Reference number: A58653; MID:89276392
 A:Accession: B58653

A:Molecule type: protein
 A:Residues: 34-61 <HIE>
 A:Experimental source: corpora cardiaca
 C:Complex: forms disulfide linked homodimers; disulfide linked heterodimers form betw
 C:Function:
 A:Description: hormone, released from the corpora cardiaca after the beginning of fl
 s an energy source

C:Superfamily: adipokine hormone
 C:Keywords: amidated carboxyl end; corpora cardiaca; heterodimer; homodimer; hormone;
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-30/Product: adipokine hormone II #status experimental <MAT1>
 F:34-61/Product: adipokine hormone-associated peptide II #status predicted <MAT2>
 F:23/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status expert
 F:30/Modified site: amidated carboxyl end (Trp) (amide in mature form from following
 F:59/Binding site: glutathione (Cys) (covalently) (partial) #status experimental
 F:59/Disulfide bonds: interchain (partial) #status experimental
 F:59/Disulfide bonds: interchain (to adipokine hormone-associated peptide I 61) (p

Query Match 1.6%; Score 7; DB 1; Length 61;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 37 TLVLVVA 43
 |||||
 DB 8 TLVLVVA 14

RESULT 8
 S04874
 hypothetical protein 73 (nifs 5' region) - Bradyrhizobium japonicum
 C:Species: Bradyrhizobium japonicum
 C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 08-Oct-1999
 C:Accession: S04874
 R:Edeling, S.
 submitted to the EMBL Data Library, December 1988
 A:Reference number: S04873
 A:Accession: S04874
 A:Molecule type: DNA
 A:Residues: 1-73 <EBE>
 A:Cross-references: EMBL:X13691; NID:g93944; PIDN:CAA31981.1; PID:g580774
 C:Genetics:
 A:Start codon: GTG

Query Match 1.6%; Score 7; DB 2; Length 73;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 38 LVLVVA 44
 |||||
 DB 62 LVLVVA 68

RESULT 9
 B81179

30s ribosomal protein S15 NMB0609 [Imported] - Neisseria meningitidis (group B strain MU
 C:Species: Neisseria meningitidis
 C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 31-Dec-2000
 C:Accession: B81179; F81926
 R:Reitel, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
 Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
 ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.
 Science 287, 1809-1815, 2000
 A:Authors: Grand, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
 A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
 A:Reference number: A81000; MUID:20175755
 A:Accession: B81179
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-89 <PRT>
 A:Cross-references: GB:AE002416; GB:AE002098; NID:g7225832; PIDN:AAF41036.1; PID:g722583
 A:Experimental source: serogroup B, strain MMD58
 R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
 ; Holroyd, S.; Jagsels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
 Nature 404, 502-506, 2000
 A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
 A:Reference number: A81775; MUID:20222556
 A:Accession: F81926
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-89 <PAR>
 A:Cross-references: GB:AL162754; GB:AL157959; NID:g7379424; PIDN:CAB84097.1; PID:g737953
 A:Experimental source: serogroup A, strain Z2491
 C:Genetics:
 A:Gene: rpsO; NMB0609; NMA0815
 C:Superfamily: Escherichia coli ribosomal protein S15; eubacterial ribosomal protein S15

Query Match 1.6%; Score 7; DB 2; Length 89;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 320 SQRRL 326
 |||||
 DB 61 SQRRL 67

RESULT 10
 C69000
 hypothetical protein MTH100 - Methanobacterium thermoautotrophicum (strain Delta H)
 C:Species: Methanobacterium thermoautotrophicum
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 04-Mar-2000
 C:Accession: C69000
 R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
 ; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
 K.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
 J. Bacteriol. 179, 7135-7155, 1997
 A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
 A:Reference number: A69000; MUID:98037514
 A:Accession: C69000
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-103 <MTH>
 A:Cross-references: GB:AE000800; GB:AE000666; NID:g2621130; PIDN:AAB84599.1; PID:g262113
 A:Experimental source: strain Delta H
 C:Genetics:
 A:Gene: MTH100
 C:Superfamily: Methanobacterium thermoautotrophicum hypothetical protein MTH100

Query Match 1.6%; Score 7; DB 2; Length 103;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 55 LITQDDL 61
 |||||
 DB 36 LITQDDL 42

RESULT 11
 B25159
 13K sin operon hypothetical protein slnr - Bacillus subtilis
 N:Alternate names: post-exponential phase transcription regulatory protein slnr
 C:Species: Bacillus subtilis
 C:Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 20-Jun-2000
 C:Accession: B25159; E69707
 R:Gaut, N.K.; Dubnau, E.; Smith, I.
 J. Bacteriol. 168, 860-869, 1986
 A:Title: Characterization of a cloned Bacillus subtilis gene that inhibits sporulatio
 A:Reference number: A91827; MUID:87056981
 A:Accession: B25159
 A:Molecule type: DNA
 A:Residues: 1-111 <GAT>
 A:Cross-references: GB:M4112; NID:g143546; PIDN:AAA22757.1; PID:g143547
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber
 C.; Bron, S.; Brouillet, S.; Burschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
 A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
 Nature 390, 249-256, 1997
 A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal
 lech, J.; Harwood, C.R.; Henauf, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M
 Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino
 A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
 Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanl
 A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se
 akuchii, M.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Tosato, V.; Uchiya
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida
 A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
 A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis
 A:Reference number: A65580; MUID:98044033
 A:Accession: E69707
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-111 <KUN>
 A:Cross-references: GB:Z99116; GB:AL009126; NID:g2634723; PIDN:CAB14392.1; PID:g26348
 A:Experimental source: strain 168
 C:Genetics:
 A:Gene: slnr
 A:Start codon: TTG
 C:Superfamily: probable transcription repressor yowR

Query Match 1.6%; Score 7; DB 2; Length 111;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 398 SVHTLLD 404
 |||||
 DB 57 SVHTLLD 63

RESULT 12
 S36284
 Ig heavy chain V region (clone alpha-FOG1-A4) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999
 C:Accession: S36284
 R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty,
 EMBO J. 12, 725-734, 1993
 A:Title: Human anti-self antibodies with high specificity from phage display library
 A:Reference number: S36256; MUID:93178448
 A:Accession: S36284
 A:Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-115 <GRI>
 A:Cross-references: EMBL:Z18826
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 1.6%; Score 7; DB 2; Length 115;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 395 R0ASVHT 401
 |||||
 DB 98 R0ASVHT 104

RESULT 13

F82716
 Hypothetical protein Xf1150 [imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa

C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000

C:Accession: F82716

R:Anonymous, The xylella fastidiosa Consortium of the Organization for Nucleotide Sequen

Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; M0ID:20365717

A>Note: for a complete list of authors see reference number A59328 below

A:Accession: F82716

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-123 <SIM>

A:Cross-references: GB:AE003950; GB:AE003849; NID:g9106104; PIDN:AAF83960.1; GSPDB:GN001

A:Experimental source: strain 9a5c

R:Simmons, A.J.G.; Relnach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carer, H

as-Neto, E.; Docena, C.; El-Dorri, H.; Facincanli, A.P.; Ferreira, A.T.S.

submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig

Chado, M.A.; Madeira, M.F.; Martins, M.V.; Marinho, C.L.; Marques, M.V.; Martins, H

A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.

, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak

A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir

M.; Teshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A:Reference number: A59328

A:Contents: annotation

C:Genetics:

A:Gene: Xf1150

Query Match 1.6%; Score 7; DB 2; Length 123;
 Best Local Similarity 100.0%; Pred. No. 39;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 211 LSGIIG 217
 |||||
 DB 104 LSGIIG 110

RESULT 14

G70813
 probable lpqs protein - Mycobacterium tuberculosis (strain H37Rv)

C:Species: Mycobacterium tuberculosis

C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000

C:Accession: G70813

R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S

; Connor, R.; Davies, R.; Devlin, K.; Feldwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A:Reference number: A70500; M0ID:98295987

A:Accession: G70813

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-130 <COL>

A:Cross-references: GB:AL022004; GB:AL123456; NID:g3261550; PIDN:CAAL7653.1; PID:g291690

A:Experimental source: strain H37Rv

A:Gene: lpqs
 C:Superfamily: Mycobacterium tuberculosis probable lpqs protein

Query Match 1.6%; Score 7; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 217 GVTVAHV 223
 |||||
 DB 14 GVTVAHV 20

RESULT 15

A27632
 T-cell receptor alpha chain precursor V region (D6) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 15-Dec-1988 #sequence_revision 30-Jun-1991 #text_change 21-Jan-2000

C:Accession: A27632

R:McElliott, D.L.; Sorger, S.B.; Matls, L.A.; Hedrick, S.M.

J. Immunol. 140, 4123-4131, 1988

A:Title: Two distinct mechanisms account for the immune response (Ir) gene control of

A:Reference number: A27632; M0ID:88229117

A:Accession: A27632

A:Molecule type: mRNA

A:Residues: 1-132 <MCE>

A:Cross-references: EMBL:M20875; NID:g201814; PIDN:AA18410.1; PID:g201815

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: T-cell receptor

E:36-109/Domain: Immunoglobulin homology <IMM>

Query Match 1.6%; Score 7; DB 2; Length 132;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 SGTKHS 189
 |||||
 DB 71 SGTKHS 77

RESULT 16

C72200
 conserved hypothetical protein - Thermotoga maritima (strain MSB8)

C:Species: Thermotoga maritima

C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000

C:Accession: C72200

R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic

Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,

C.M.

Nature 399, 323-329, 1999

A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome

A:Reference number: A72200; M0ID:99287316

A:Accession: C72200

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-132 <ARN>

A:Cross-references: GB:AE001824; GB:AE000512; NID:g4982455; PIDN:AAD36934.1; PID:g498

A:Experimental source: strain MSB8

C:Genetics:

A:Gene: TM1872

C:Superfamily: hypothetical protein MJ1081

Query Match 1.6%; Score 7; DB 2; Length 132;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 431 LEGNADS 437
 |||||
 DB 78 LEGNADS 84

RESULT 17

S56158

Cytochrome oxidase chain 2 - Sulfolobus acidocaldarius

C:Species: Sulfolobus acidocaldarius

C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 26-Aug-1999

C:Accession: S56158

R:Castresana, J.; Luebben, M.; Saraste, M.

J. Mol. Biol. 250, 202-210, 1995.

A:Title: New archaeobacterial genes coding for redox proteins: implications for the evolution

A:Reference number: S56155, M01D:95533177

A:Accession: S56158

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-146 <CDS>

A:Cross-references: EMBL:Z48338; NID:9927521; PID:9927526

F:92,127,131,138/Binding site: copper_1 (His, Cys, Cys, Met) #status predicted

F:127,129,131,135/Binding site: copper_2 (Cys, Glu, Cys, His) #status predicted

Query Match

1.6%; Score 7; DB 2; Length 146;

Best Local Similarity 100.0%; Pred. No. 45;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 221 AAVVLIV 227

DB 15 AAVVLIV 21

RESULT 18

T36081

Probable integral membrane protein - Streptomyces coelicolor

C:Species: Streptomyces coelicolor

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 08-Sep-2000

C:Accession: T36081

R:Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, April 1999

A:Reference number: Z21573

A:Accession: T36081

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-151 <CDS>

A:Cross-references: EMBL:AL049630; PIDN:CAB40933.1; GSPDB:GN00070; SCOEDB:SCEI26.11

A:Experimental source: strain A3(2)

C:Genetics:

A:Gene: SCOEDB:SCEI26.11

C:Superfamily: Streptomyces coelicolor probable integral membrane protein SCEI26.11

Query Match

1.6%; Score 7; DB 2; Length 151;

Best Local Similarity 100.0%; Pred. No. 46;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 219 TVAAVVL 225

DB 25 TVAAVVL 31

RESULT 19

T03898

hypothetical protein R09E12.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999

C:Accession: T03898

R:Blanchard, M.; Elliott, G.; Keppler, D.; Smith, A.

submitted to the EMBL Data Library, July 1997

A:Reference number: Z15130

A:Accession: T03898

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-165 <BLA>

A:Cross-references: EMBL:AF016422; NID:g2291187; PIDN:AAB65315.1; PID:g2291191

C:Genetics:

A:Map position: V

A:Note: R09E12.4

C:Superfamily: Caenorhabditis elegans hypothetical protein R09E12.4

Query Match

1.6%; Score 7; DB 2; Length 165;

Best Local Similarity 100.0%; Pred. No. 50;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 215 IIGVYA 221

DB 135 IIGVYA 141

RESULT 20

NCBBPX

Micrococcal nuclease (EC 3.1.31.1) precursor - Shigella flexneri plasmid psa

C:Species: Shigella flexneri

C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 11-Jun-1999

C:Accession: S20541

R:Close, S.M.; Kado, C.I.

Mol. Microbiol. 6, 521-527, 1992

A:Title: A gene near the plasmid psa origin of replication encodes a nuclease.

A:Reference number: S20540; M01D:92219997

A:Accession: S20541

A:Molecule type: DNA

A:Residues: 1-174 <CDS>

A:Cross-references: GB:U30471; EMBL:M01325; NID:g976151; PIDN:AAA75246.1; PID:g976155

C:Genetics:

A:Gene: nuc

A:Genome: plasmid

C:Superfamily: micrococcal nuclease

C:Keywords: hydrolase

F:1-25/Domain: signal sequence #status predicted <SIG>

F:26-174/Product: micrococcal nuclease #status predicted <MAT>

Query Match

1.6%; Score 7; DB 1; Length 174;

Best Local Similarity 100.0%; Pred. No. 52;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 221 AAVVLIV 227

DB 13 AAVVLIV 19

RESULT 21

F70653

probable bfrB protein - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000

C:Accession: F70653

R:Coile, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon

; Connor, R.; Davies, R.; Devlin, K.; Fellwell, T.; Gentles, S.; Hamlin, N.; Holroyd,

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno

A:Reference number: A70500; M01D:98295987

A:Accession: F70653

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-181 <CDS>

A:Cross-references: GB:Z83864; GB:AL123456; NID:g3261687; PIDN:CAB06225.1; PID:g17811

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: bfrB

C:Superfamily: ferritin

Query Match

1.6%; Score 7; DB 2; Length 181;

Best Local Similarity 100.0%; Pred. No. 54;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 APAASGA 14
|||||||
Db 167 APAASGA 173

RESULT 22

T47408
lipid-transfer-like protein - Arabidopsis thaliana
N:Alternate names: protein T28A8.10
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: T47408
R:Purnelle, B.; Boutry, M.; Goffeau, A.; Mewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X
submitted to the Protein Sequence Database, March 2000
A:Reference number: 224466
A:Accession: T47408
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-193 <PUR>
A:Cross-references: EMBL:AL162691
C:Genetics:
A:Map position: 3
A:Introns: 122/1; 149/1
A>Note: T28A8.10

Query Match 1.6%; Score 7; DB 2; Length 193;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 222 AVLIVA 228
|||||||
Db 8 AVLIVA 14

RESULT 23

NAD(P)H oxidoreductase homolog ydeQ - Bacillus subtilis
C:Species: Bacillus subtilis
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C:Accession: C69779
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berta
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, C.D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizi, A.; Gall
lech, J.; Harwood, C.R.; Henauf, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A.; Authers: lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue
Y, M.; Ogawa, K.; Ogihara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetell
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon
A:Authors: Schleich, S.; Schroeter, R.; Scofield, F.; Sekiguchi, J.; Sekowska, A.; Seron
A:Authors: Schleich, S.; Schroeter, R.; Scofield, F.; Sekiguchi, J.; Sekowska, A.; Seron
T.; Winters, P.; Wipet, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033
A:Accession: C69779
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-197 <GEN>
A:Cross-references: GB:299106; GB:AL009126; NID:g2632653; PIDN:CAB12337.1; PID:g2632830
A:Experimental source: strain 168
C:Genetics:
A:Gene: ydeQ
C:Superfamily: NAD(P)H dehydrogenase (quinone) 2

Query Match 1.6%; Score 7; DB 2; Length 197;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 36 KTLVLV 42
|||||||
Db 5 KTLVLV 11

RESULT 24

T21587
peptidylprolyl isomerase (EC 5.2.1.8) F31C3.1 (similarity) - Caenorhabditis elegans
N:Contents: cyclophilin
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
C:Accession: T21587
R:Cottage, A.
submitted to the EMBL Data Library, March 1997
A:Reference number: 219446
A:Accession: T21587
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-204 <WIL>
A:Cross-references: EMBL:292784; PIDN:CAB07192.1; GSPDB:GN00019; CESP:F31C3.1
A:Experimental source: clone F31C3
C:Genetics:
A:Gene: CESP:F31C3.1
A:Map position: 1
A:Introns: 69/3
C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
C:Keywords: cis-trans-isomerase
F:28-190/domain: cyclophilin homology <CYP>

Query Match 1.6%; Score 7; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 40 LVVAVL 46
|||||||
Db 5 LVVAVL 11

RESULT 25

S27736
hypothetical protein B - Thermus aquaticus
C:Species: Thermus aquaticus
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 08-Oct-1999
C:Accession: S27736
R:Ashby, M.K.; Bergquist, P.L.
submitted to the EMBL Data Library, July 1990
A:Description: Cloning and sequence of IS1000 from Thermus thermophilus HB8.
A:Reference number: S27735
A:Accession: S27736
A:Molecule type: DNA
A:Residues: 1-213 <NSH>
A:Cross-references: EMBL:M3159; NID:g155103; PIDN:AA27494.1; PID:g295398
A>Note: the source is designated as Thermus thermophilus
C:Genetics:
A:Start codon: GTG

Query Match 1.6%; Score 7; DB 2; Length 213;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 322 RRRLLVP 328
|||||||
Db 99 RRRLLVP 105

RESULT 26

S70837
pilo protein - Neisseria gonorrhoeae
C:Species: Neisseria gonorrhoeae
C>Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 08-Oct-1999

C:Accession: S70837
R:Drake, S.L.; Koomey, M.
Mol. Microbiol. 18, 975-986, 1995
A:Title: The product of the pilO gene is essential for the biogenesis of type IV pili in
A:Reference number: S70837; MID:96422484
A:Accession: S70837
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-215 <DRA>
A:Cross-references: EMBL:U40596; NID:g1173872; PIDN:AAC43601.1; PID:g1173873
A:Experimental source: strain MS11
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1995
C:Genetics:
A:Gene: pilO

Query Match 1.6%; Score 7; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 40 LVYAAVL 46
|||||
DB 29 LVYAAVL 35

RESULT 27
S71464
ribonuclease (EC 3.1.-.-) S5 - Antirrhinum hispanicum
N:Alternate names: S-Locus RNase; self incompatibility-associated protein S5
C:Species: Antirrhinum hispanicum
C:Date: 09-Dec-1997 #sequence_revision 09-Dec-1997 #text_change 20-Jun-2000
C:Accession: S71464
R:Xue, Y.; Carpenter, R.; Dickinson, H.G.; Coen, E.S.
Plant Cell 8, 805-814, 1996
A:Title: Origin of allelic diversity in antirrhinum S locus RNases.
A:Reference number: S71464; MID:96240018
A:Accession: S71464
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-233 <XUE>
A:Cross-references: EMBL:X96464; NID:g1405427; PIDN:CA65318.1; PID:g1405428
C:Superfamily: Enterobacter ribonuclease
C:Keywords: hydrolase

Query Match 1.6%; Score 7; DB 2; Length 233;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 393 TGRDASV 399
|||||
DB 203 TGRDASV 209

RESULT 28
H75392
hypothetical protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C:Accession: H75392
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uitterback, T.; Zalewski, C.; Mc
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MID:20036896
A:Accession: H75392
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-238 <WHI>
A:Cross-references: GB:AE001990; GB:AE000513; NID:96459214; PIDN:AAF11027.1; PID:9645921
A:Experimental source: strain R1
C:Genetics:

A:Gene: DR1454
A:Map position: 1

Query Match 1.6%; Score 7; DB 2; Length 238;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 403 LDALETL 409
|||||
DB 8 LDALETL 14

RESULT 29
G81255
N-(5'-phospho-D-ribosylformimino)-5-amino-1-(5'-phosphoribosyl)-4-imidazolecarboxami
C:Species: Campylobacter jejuni
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jun-2000
C:Accession: G81255
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Kelley, J.M.; Churcher, C.; Basham, D.; Chil
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; Vanyilet, A.; Whitehead, S.; Ba
Nature 403, 665-668, 2000
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals
A:Reference number: A81250; MID:20150912
A:Accession: G81255
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-243 <PAR>
A:Cross-references: GB:AL139079; GB:AL111168; NID:96968971; PIDN:CAB73589.1; PID:9696
A:Experimental source: serotype O2, strain NCYC 11168
C:Genetics:
A:Gene: hnsA; Cj1601
C:Superfamily: N-(5'-phospho-D-ribosylformimino)-5-amino-1-(5'-phosphoribosyl)-4-im
C:Keywords: intramolecular oxidoreductase; isomerase

Query Match 1.6%; Score 7; DB 2; Length 243;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 244 LKGCISG 250
|||||
DB 214 LKGCISG 220

RESULT 30
S44914
ZK688.7 protein - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Sep-1997
C:Accession: S44914
R:Wilson, R.
submitted to the EMBL Data Library, May 1993
A:Description: Sequence of the C. elegans cosmid ZK688.
A:Reference number: S44913
A:Accession: S44914
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-243 <WIL>
A:Cross-references: EMBL:L16621; NID:g289775; PID:g289777
C:Genetics:
A:Introns: 23/3; 109/3; 167/1

Query Match 1.6%; Score 7; DB 2; Length 243;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 131 TTRNTVC 137
|||||
DB 142 TTRNTVC 148

RESULT 31
A69013
conserved hypothetical protein MTH1099 - Methanobacterium thermoautotrophicum (strain De
C:Species: Methanobacterium thermoautotrophicum
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C:Accession: A69013
R:Smith, D.R.; Doucette-Stamm, L.A.; Delouhery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
; Qiu, D.; Spadafora, R.; Vicalire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
K.I.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A:Reference number: A69000; MUID:98037514
A:Accession: A69013
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-246 <MTH>
A:Cross-references: GB:AE000880; GB:AE000666; NID:92622192; PIDN:AAB85588.1; PID:9262220
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH1099
A:Start codon: GTG

Query Match 1.6%; Score 7; DB 2; Length 246;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 44 AVLLVS 50
|||||||
Db 44 AVLLVS 50

RESULT 32
D69065
conserved hypothetical protein MTH1489 - Methanobacterium thermoautotrophicum (strain De
C:Species: Methanobacterium thermoautotrophicum
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C:Accession: D69065
R:Smith, D.R.; Doucette-Stamm, L.A.; Delouhery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
; Qiu, D.; Spadafora, R.; Vicalire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
K.I.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A:Reference number: A69000; MUID:98037514
A:Accession: D69065
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-249 <MTH>
A:Cross-references: GB:AE000909; GB:AE000666; NID:92622596; PIDN:AAB85964.1; PID:9262260
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH1489

Query Match 1.6%; Score 7; DB 2; Length 249;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 405 ALETLGE 411
|||||||
Db 123 ALETLGE 129

RESULT 33
C72572
hypothetical protein APE1860 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jun-2000
C:Accession: C72572
R:Kawababayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Hatakeyama, Y.; Jin-no, K.; Takah
awa, H.; Takamizawa, Y.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyd

A:Reference number: A72450; MUID:99310339
A:Accession: C72572
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-251 <KAW>
A:Cross-references: DDBJ:AP000062; NID:95105244; PIDN:BA80864.1; PID:dl044650; PID:g
A:Experimental source: strain K1
C:Genetics:
A:Gene: APE1860
C:Superfamily: Aeropyrum pernix hypothetical protein APE1860

Query Match 1.6%; Score 7; DB 2; Length 251;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 42 VAAVLL 48
|||||||
Db 222 VAAVLL 228

RESULT 34
F83933
ABC transporter (ATP-binding protein) BH2270 [imported] - Bacillus halodurans (strain
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 31-Dec-2000
C:Accession: F83933
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
A:Reference number: A83650; MUID:20263314
A:Accession: F83933
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-261 <TNO>
A:Cross-references: GB:AP001515; GB:BA000004; NID:910174886; PIDN:BA805989.1; GSPDB:G
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH2270
C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homolog

Query Match 1.6%; Score 7; DB 2; Length 261;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 370 VAKAEAA 376
|||||||
Db 122 VAKAEAA 128

RESULT 35
A82578
glycerol uptake facilitator protein XF2267 [imported] - Xylella fastidiosa (strain 9a
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C:Accession: A82578
R:anonymous, The Xylella fastidiosa Consortium of the organization for Nucleotide Seq
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: A82578
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-275 <SIM>
A:Cross-references: GB:AE004039; GB:AE003849; NID:99107425; PIDN:AAF85066.1; GSPDB:GN
A:Experimental source: strain 9a5c
R:Stimpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.
Bionese, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Canario, L.E.A.; Carraro, D.M.; Carre
as-Neto, E.; Docena, C.; El-Doroty, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to Genbank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr

J.D.; Jungueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigle, M.A.; Madeira, A.M.B.N.; Madeira, R.M.F.; Martino, C.L.; Marques, M.V.; Martins, E.A.; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak, A.; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira, M.; Teshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF2267
C:Superfamily: glycerol facilitator protein

Query Match 1.6%; Score 7; DB 2; Length 275;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 237 WKKVLPY 243
|||||||
DB 84 WKKVLPY 90

RESULT 36
E49539
xyloglucan endo-1,4-beta-D-glucanase (EC 3.2.1.-) - wheat
C:Species: Triticum aestivum (common wheat)
C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
C:Accession: E49539
R:Okazawa, K.; Sato, Y.; Nakagawa, T.; Asada, K.; Kato, I.; Tomita, E.; Nishitani, K.
J. Biol. Chem. 268, 25364-25368, 1993
A:Title: Molecular cloning and cDNA sequencing of endoxylglucan transferase, a novel cl
A:Reference number: A49539; M0ID:94064597
A:Accession: E49539
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-293 <OKA>
A:Cross-references: GB:DI6457; NID:q457573; PIDN:BA003924.1; PID:q469511
A:Note: sequence extracted from NCBI backbone (NCBIP:13915)
C:Superfamily: endoxylglucan transferase
C:Keywords: glycosidase; hydrolase

Query Match 1.6%; Score 7; DB 2; Length 293;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 41 VVAAYLL 47
|||||||
DB 11 VVAAYLL 17

RESULT 37
H64783
carbamate kinase (EC 2.7.2.2) - Escherichia coli
C:Species: Escherichia coli
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: H64783
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; M0ID:97426617
A:Accession: H64783
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-297 <BLAT>
A:Cross-references: GB:AE000158; GB:U00096; NID:g1786728; PIDN:AACT3623.1; PID:g1786732;
A:Experimental source: strain K-12, substrain MG1655
C:Genetics:
A:Gene: arcQ; ybcF
C:Superfamily: carbamate kinase

C:Keywords: phosphotransferase

Query Match 1.6%; Score 7; DB 1; Length 297;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 247 ICSGGG 253
|||||||
DB 180 ICSGGG 186

RESULT 38
F69203
5-methyltetrahydropteroylirriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14)
N:Alternate names: cobalamin-independent methionine synthase
C:Species: Methanobacterium thermoautotrophicum
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 24-Sep-1999
C:Accession: F69203
R:Smith, D.R.; Doucette-Stamm, L.A.; Delonghery, C.; Lee, H.; Dubois, J.; Aldredge, T
; Qiu, D.; Spadafora, R.; Vitale, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jivani,
K.; S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: fu
A:Reference number: A69000; M0ID:98037514
A:Accession: F69203
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-308 <MTB>
A:Cross-references: GB:AE000856; GB:AE000666; NID:g2621862; PIDN:AAB85278.1; PID:g262
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH775
A:Start codon: GTG
C:Superfamily: 5-methyltetrahydropteroylirriglutamate--homocysteine S-methyltransferas
C:Keywords: methyltransferase

Query Match 1.6%; Score 7; DB 2; Length 308;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 407 ETLGERL 413
|||||||
DB 17 ETLGERL 23

RESULT 39
G70330
ADPglyceromanno-heptose 6-epimerase (EC 5.1.3.20) rfad [similarity] - Aquifex aeolicu
C:Species: Aquifex aeolicus
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 28-Jul-2000
C:Accession: G70330
R:Deckerl, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;
V.
Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; M0ID:98196666
A:Accession: G70330
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-310 <AQF>
A:Cross-references: GB:AE000684; NID:g2983009; PIDN:AA06623.1; PID:g2983012; GB:AE00
C:Experimental source: strain VF5
C:Genetics:
A:Gene: rfad
C:Superfamily: ADPglyceromanno-heptose 6-epimerase; UDPglucose 4-epimerase homology
C:Keywords: isomerase
F:3-310/Domain: UDPglucose 4-epimerase homology <UDP>

Query Match 1.6%; Score 7; DB 1; Length 310;
Best Local Similarity 100.0%; Pred. No. 85;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 273 NEIVSIL 279
|||||||
Db 244 NEIVSIL 250

RESULT 40

S30173
probable mercuric ion transport protein merx - Streptomyces lividans
C:Species: Streptomyces lividans
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 22-Oct-1999
C:Accession: S30173; S23613
R:Sedlmeyer, R.; Altenbuchner, J.
Mol. Gen. Genet. 236, 76-85, 1992
A:Title: Cloning and DNA sequence analysis of the mercury resistance genes of Streptomyces lividans
A:Reference number: S30168; MUID:93156687
A:Accession: S30173
A:Molecule type: DNA
A:Residues: 1-319 <ALT>
A:Cross-references: EMBL:X65467; NID:947180; PIDN:CAA46465.1; PID:947186
A:Experimental source: strain 1326
C:Genetics:
A:Gene: merx
C:Function:
A:Description: probably involved in mercuric ion transport.
A:Pathway: mercury resistance
A:Note: mercury resistance operon
C:Keywords: mercury transport; transmembrane protein
F:84-100/Domain: transmembrane #status predicted <TM1>
F:135-151/Domain: transmembrane #status predicted <TM2>
F:175-191/Domain: transmembrane #status predicted <TM3>
F:256-272/Domain: transmembrane #status predicted <TM4>

Query Match 1.6%; Score 7; DB 2; Length 319;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 AAVLLV 49
|||||||
Db 174 AAVLLV 180

RESULT 41

H83746
acetoaldehyde dehydrogenase (TPP-dependent) alpha chain BH0776 [imported] - Bacillus halodurans
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 31-Dec-2000
C:Accession: H83746
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: AB3650; MUID:20263314
A:Accession: H83746
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-326 <STO>
A:Cross-references: GB:AP001509; GB:BA000004; NID:910171376; PIDN:BA04495.1; GSPDB:GNOC
A:Experimental source: strain C-125.
C:Genetics:
A:Gene: BH0776
C:Superfamily: pyruvate dehydrogenase (lipoamide) alpha chain; thiamin pyrophosphate-dir

Query Match 1.6%; Score 7; DB 2; Length 326;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 414 AKOKIED 420
|||||||
Db 298 AKOKIED 304

RESULT 42

A59241
DNA-directed DNA polymerase (EC 2.7.7.7) III delta chain homolog [imported] - Pseudomonas aeruginosa
C:Species: Pseudomonas aeruginosa
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 19-May-2000
C:Accession: A59241
R:Alm, R.A.; Bodero, A.J.; Free, P.D.; Mattick, J.S.
J. Bacteriol. 178, 46-53, 1996
A:Title: Identification of a novel gene, pilZ, essential for type 4 fimbrial biogenesis
A:Reference number: A59241; MUID:96125227
A:Accession: A59241
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-326 <Alm>
A:Cross-references: GB:I42622; NID:9972777; PIDN:AA03518.1; PID:9972778
A:Experimental source: strain PA01; clone PAB31
C:Genetics:
A:Gene: hoiB
C:Superfamily: DNA-directed DNA polymerase III delta' chain
C:Keywords: nucleotidyltransferase

Query Match 1.6%; Score 7; DB 2; Length 326;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 311 LLEPAEA 317
|||||||
Db 109 LLEPAEA 115

RESULT 43

D83275
DNA polymerase III, delta prime subunit PA2961 [imported] - Pseudomonas aeruginosa (S
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: D83275
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Muzoguchi, S.D.; Warrenner, P.; Hickey, M.J.;
Adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lathig, K.; L
.. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A:Reference number: AB2950; MUID:20437337
A:Accession: D83275
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-328 <STO>
A:Cross-references: GB:AE004722; GB:AE004091; NID:99949054; PIDN:AA06349.1; GSPDB:GN
A:Experimental source: strain PA01
C:Genetics:
A:Gene: hoiB; PA2961
C:Superfamily: DNA-directed DNA polymerase III delta' chain

Query Match 1.6%; Score 7; DB 2; Length 328;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 311 LLEPAEA 317
|||||||
Db 111 LLEPAEA 117

RESULT 44

D71887
ADPGlyceramano-heptose 6-epimerase (EC 5.1.3.20) gmbd homolog [similarity] - Helicob
C:Species: Helicobacter pylori
A:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 28-Jul-2000
C:Accession: D71887
R:Alm, R.A.; Ling, L.S.L.; Molr, D.T.; King, B.L.; Brown, E.D.; Dolg, P.C.; Smith, D.
; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, O.; Taylor, D.E.; Vovis, G.F

Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A:Reference number: A71800; MUID:99120537
A:Accession: D71887
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-339 <ARN>
A:Cross-references: GB:AE001509; GB:AE001439; NID:g4155350; PIDN:AAD06369.1; PID:g415535
A:Experimental source: strain J99
A:Genetics:
A:Gene: gmbd
C:Superfamily: ADPglyceromanno-heptose 6-epimerase; UDPglucose 4-epimerase homology
C:Keywords: isomerase

Query Match 1.6%; Score 7; DB 2; Length 339;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 273 NEIVSIL 279
|||||
DB 261 NEIVSIL 267

RESULT 45
C64627
ADPglyceromanno-heptose 6-epimerase (EC 5.1.3.20) HP0859 [similarity] - Helicobacter pylori
C:Species: Helicobacter pylori
C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 28-Jul-2000
C:Accession: C64627
R:Tom, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, R.; Richardson, D.; Dodson, R.; Khaliq, H.G.; Gilek, A.; McKenney, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Matthey, L.; Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karp, P.D.; Smith, H.O.; Fraser, C.
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:97394467
A:Accession: C64627
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-330 <OM>
A:Cross-references: GB:AE000596; GB:AE000511; NID:g2313982; PIDN:AAD07905.1; PID:g231399
C:Superfamily: ADPglyceromanno-heptose 6-epimerase; UDPglucose 4-epimerase homology
C:Keywords: isomerase

Query Match 1.6%; Score 7; DB 2; Length 330;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 273 NEIVSIL 279
|||||
DB 262 NEIVSIL 268

RESULT 46
JC2329
translation initiation factor eIF-2 beta chain - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 08-Oct-1999
C:Accession: JC2329; PC2209; S38536
R:Welsh, G.I.; Price, N.T.; Bladergroen, B.A.; Bloomberg, G.; Proud, C.G.
Biochem. Biophys. Res. Commun. 201, 1279-1288, 1994
A:Title: Identification of novel phosphorylation sites in the beta-subunit of translatio
A:Reference number: JC2329; MUID:94296400
A:Accession: JC2329
A:Molecule type: mRNA
A:Residues: 1-333 <WEL>
A:Accession: PC2209
A:Molecule type: protein
A:Residues: 25-38;121-149;205-233 <WE2>
R:Price, N.T.; Hall, L.; Proud, C.G.
Biochim. Biophys. Acta 1216, 170-172, 1993

A:Title: Cloning of cDNA for the beta-subunit of rabbit translation initiation factor
A:Reference number: S38536; MUID:94032484
A:Accession: S38536
A:Molecule type: mRNA
A:Residues: 1-38, 'L', '40-333 <PRI>
A:Cross-references: EMBL:X73836; NID:g415860; PIDN:CAA52058.1; PID:g415861
C:Superfamily: human translation initiation factor eIF-2 beta chain
C:Keywords: phosphoprotein
F:2,6/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status experim
F:13/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status experim
F:218/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status exp

Query Match 1.6%; Score 7; DB 2; Length 333;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 291 VOEPAP 297
|||||
DB 107 VOEPAP 113

RESULT 47
C81801
ketol-acid reductoisomerase (EC 1.1.1.86) NMA1763 [imported] - Neisseria meningitidis
C:Species: Neisseria meningitidis
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jun-2000
C:Accession: C81801
R:Parhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo
; Holtroyd, S.; Jagsels, K.; Leather, S.; Moule, S.; Kungall, K.; Quail, M.A.; Rajandre
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491
A:Reference number: A81775; MUID:20222556
A:Accession: C81801
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-337 <PAR>
A:Cross-references: GB:AL162757; GB:AL157959; NID:g7380371; PIDN:CAB84991.1; PID:g738
A:Experimental source: serogroup A, strain 22491
C:Genetics:
A:Gene: ilvC; NMA1763
C:Superfamily: Methanococcus ketol-acid reductoisomerase; ketol-acid reductoisomerase
C:Keywords: intramolecular transferase; isomerase; oxidoreductase
F:20-201/Domain: ketol-acid reductoisomerase homology <KAR>

Query Match 1.6%; Score 7; DB 2; Length 337;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 372 KAEAGH 378
|||||
DB 54 KAEAGH 60

RESULT 48
F81066
ketol-acid reductoisomerase NMB1574 [imported] - Neisseria meningitidis (group B stra
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 31-Dec-2000
C:Accession: F81066
R:Rettelio, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen,
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.
rl, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignanl, V.; Pizza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.;
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: AB1000; MUID:20175755
A:Accession: F81066
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-337 <RET>
A:Cross-references: GB:AE002508; GB:AE002098; NID:g7226820; PIDN:AAF41927.1; PID:g722

A:Experimental source: serogroup B, strain MMD58
 C:Genetics:
 A:Gene: NMBL1574
 C:Superfamily: Methanococcus ketol-acid reductoisomerase; ketol-acid reductoisomerase hc
 F:20-201/Domain: ketol-acid reductoisomerase homology <R>

Query Match 1.6%; Score 7; DB 2; Length 337;
 Best Local Similarity 100.0%; Pred. No. 91;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 372 KAEAGH 378
 |||||
 Db 54 KAEAGH 60

RESULT 49
 A82502
 oxidoreductase, Gfo/Ith/Moa family VCA0099 [imported] - vibrio cholerae (group O1 strain
 C:Species: Vibrio cholerae
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 15-Sep-2000
 C:Accession: A82502
 R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;
 chardson, D.; Ermolaeva, M.D.; Yamatchev, J.; Bass, S.; Qin, H.; Dragoli, I.; Sellers, F.
 1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A>Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
 A:Reference number: A82035; MIMD:20406833
 A:Accession: A82502
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-346 <HEI>
 A:Cross-references: GB:AE004352; GB:AE003853; NID:9657475; PIDN:AAF96013.1; GSPDB:GN001
 A:Experimental source: serogroup O1; strain N16961; biotype El Tor
 C:Genetics:
 A:Gene: VCA0099
 A:Map position: 2
 C:Superfamily: conserved hypothetical protein b1624

Query Match 1.6%; Score 7; DB 2; Length 346;
 Best Local Similarity 100.0%; Pred. No. 93;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 49 VSAESAL 55
 |||||
 Db 317 VSAESAL 323

RESULT 50
 I50107
 MHC class I histocompatibility antigen UBA*01 precursor - zebra fish
 C:Species: Brachydanio rerio (zebra fish)
 C:Date: 13-Mar-1997 #sequence_revision 13-Mar-1997 #text_change 03-Dec-1999.
 C:Accession: I50107; S49817
 R:Takeuchi, H.; Figueroa, F.; O'Huigin, C.; Klein, J.
 Immunogenetics 42, 77-84, 1995
 A>Title: Cloning and characterization of class I Mhc genes of the zebrafish, Brachydanio
 A:Reference number: I50106; MIMD:95331830
 A:Accession: I50107
 A:Status: Preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-346 <RA>
 A:Cross-references: EMBL:Z46777; NID:9577535; PIDN:CAA86732.1; PID:9577536
 C:Genetics:
 A:Gene: UBA*01
 C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 1.6%; Score 7; DB 2; Length 348;
 Best Local Similarity 100.0%; Pred. No. 94;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 41 VVAAYLL 47
 |||||
 Db 307 VVAAYLL 313

Search completed: May 23, 2001, 14:21:39
 Job time: 108 sec

